

SEQUENCE LISTING

<110> Shimkets, Richard A.

<120> NOVEL NUCLEIC ACID SEQUENCES ENCODING HUMAN SLIT-,
MEGF-, AND ROUNDABOUT-LIKE POLYPEPTIDES

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<140> 09/991,053

<141> 2001-11-21

<150> USSN 60/123,667

<151> 1999-03-09

<150> 09/520,781

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<170> PatentIn Ver. 2.1

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Trp	Thr	Pro	Val	Pro	Asp	Glu	Arg	Val	Pro	Lys	Pro	Arg	Pro	Gly	Cys	
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Cys	Ala	Gly	Ser	Ser	Ser	Leu	Glu	Arg	Tyr	Ala	Thr	Ser	Asn	Glu	Phe	370	375	380
Pro	Asp	Asp	Thr	Leu	Asn	Phe	Ile	Lys	Thr	His	Pro	Leu	Met	Asp	Glu	385	390	395
Ala	Val	Pro	Ser	Ile	Phe	Asn	Arg	Pro	Trp	Phe	Leu	Arg	Thr	Met	Val	405	410	415
Arg	Tyr	Arg	Leu	Thr	Lys	Ile	Ala	Val	Asp	Thr	Ala	Ala	Gly	Pro	Tyr	420	425	430
Gln	Asn	His	Thr	Val	Val	Phe	Leu	Gly	Ser	Glu	Lys	Gly	Ile	Ile	Leu	435	440	445
Lys	Phe	Leu	Ala	Arg	Ile	Gly	Asn	Ser	Gly	Phe	Leu	Asn	Asp	Ser	Leu	450	455	460
Phe	Leu	Glu	Glu	Met	Ser	Val	Tyr	Asn	Ser	Glu	Lys	Cys	Ser	Tyr	Asp	465	470	475
Gly	Val	Glu	Asp	Lys	Arg	Ile	Met	Gly	Met	Gln	Leu	Asp	Arg	Ala	Ser	485	490	495
Ser	Ser	Leu	Tyr	Val	Ala	Phe	Ser	Thr	Cys	Val	Ile	Lys	Val	Pro	Leu	500	505	510
Gly	Arg	Cys	Glu	Arg	His	Gly	Lys	Cys	Lys	Lys	Thr	Cys	Ile	Ala	Ser	515	520	525
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Ala	Ile	Leu	Thr	Pro	Leu	Met	His	Asn	Gly	Lys	Leu	Ala	Thr	Pro	Gly	725	730	735
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Thr	Asp	Leu	Pro	Leu	Arg	Ala	Ser	Pro	Ser	His	Ile	Pro	Ser	Val	Val	805	810	815
Val	Leu	Pro	Ile	Thr	Gln	Gln	Gly	Tyr	Gln	His	Glu	Tyr	Val	Asp	Gln	820	825	830
Pro	Lys	Met	Ser	Glu	Val	Ala	Gln	Met	Ala	Leu	Glu	Asp	Gln	Ala	Ala	835	840	845
Thr	Leu	Glu	Tyr	Lys	Thr	Ile	Lys	Glu	His	Leu	Ser	Ser	Lys	Ser	Pro	850	855	860
Asn	His	Gly	Val	Asn	Leu	Val	Glu	Asn	Leu	Asp	Ser	Leu	Pro	Pro	Lys	865	870	875
Val	Pro	Gln	Arg	Glu	Ala	Ser	Leu	Gly	Pro	Pro	Gly	Ala	Ser	Leu	Ser	885	890	895
Gln	Thr	Gly	Leu	Ser	Lys	Arg	Leu	Glu	Met	His	His	Ser	Ser	Ser	Tyr	900	905	910
Gly	Val	Asp	Tyr	Lys	Arg	Ser	Tyr	Pro	Thr	Asn	Ser	Leu	Thr	Arg	Ser	915	920	925
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cgctgtacca gttcgctccg agccccggcc gcctgtccgt cgatgcaccg aaaaggggtga 180
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Met Arg Ser Glu Ala Leu Leu
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Leu Tyr Phe Thr Leu Leu His Phe Ala Gly Ala Gly Phe Pro Glu Asp
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Ser Glu Pro Ile Ser Ile Ser His Gly Asn Tyr Thr Lys Gln Tyr Pro
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Val Phe Val Gly His Lys Pro Gly Arg Asn Thr Thr Gln Arg His Arg
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Leu Asp Ile Gln Met Ile Met Ile Met Asn Gly Thr Leu Tyr Ile Ala
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Ala Arg Asp His Ile Tyr Thr Val Asp Ile Asp Thr Ser His Thr Glu
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Val Asp Thr Cys Arg Met Lys Gly Lys His Lys Asp Glu Cys His Asn
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Phe Ile Lys Val Leu Leu Lys Lys Asn Asp Asp Ala Leu Phe Val Cys
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Gly Thr Asn Ala Phe Asn Pro Ser Cys Arg Asn Tyr Lys Met Asp Thr
140 145 150

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Leu Glu Pro Phe Gly Asp Glu Phe Ser Gly Met Ala Arg Cys Pro Tyr	
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Ser Leu Gly Glu Ser Pro Thr Leu Arg Thr Val Lys His Asp Ser Lys	
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Arg Leu Asn Cys Ser Val Pro Gly Asp Ser His Phe Tyr Phe Asn Ile	
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Cys Ala Tyr Asp Met Leu Asp Ile Ala Ser Val Phe Thr Gly Arg Phe	
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Lys Glu Gln Lys Ser Pro Asp Ser Thr Trp Thr Pro Val Pro Asp Glu	
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Arg Val Pro Lys Pro Arg Pro Gly Cys Cys Ala Gly Ser Ser Ser Leu	
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gaa aga tat gca acc tcc aat gag ttc cct gat gat acc ctg aac ttc	1386

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Ile	Lys	Thr	His	Pro	Leu	Met	Asp	Glu	Ala	Val	Pro	Ser	Ile	Phe	Asn		
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Asn	Ser	Gly	Phe	Leu	Asn	Asp	Ser	Leu	Phe	Leu	Glu	Glu	Met	Ser	Val		
				460					465					470			
tac	aac	tct	gaa	aaa	tgc	agc	tat	gat	gga	gtc	gaa	gac	aaa	agg	atc	1674	
Tyr	Asn	Ser	Glu	Lys	Cys	Ser	Tyr	Asp	Gly	Val	Glu	Asp	Lys	Arg	Ile		
			475					480					485				
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Met	Gly	Met	Gln	Leu	Asp	Arg	Ala	Ser	Ser	Ser	Leu	Tyr	Val	Ala	Phe		
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Ser	Thr	Cys	Val	Ile	Lys	Val	Pro	Leu	Gly	Arg	Cys	Glu	Arg	His	Gly		
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Lys	Cys	Lys	Lys	Thr	Cys	Ile	Ala	Ser	Arg	Asp	Pro	Tyr	Cys	Gly	Trp		
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Ile	Lys	Glu	Gly	Gly	Ala	Cys	Ser	His	Leu	Ser	Pro	Asn	Ser	Arg	Leu		
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Cys	His	Asn	Ser	Phe	Val	Ala	Leu	Asn	Gly	Val	Ile	Arg	Glu	Ser	Tyr		
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ctc	aaa	ggc	cac	gac	cag	ctg	gtt	ccc	gtc	acc	ctc	ttg	gcc	att	gca	2010	
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gtc	atc	ctg	gct	ttc	gtc	atg	ggg	gcc	gtc	ttc	tcg	ggc	atc	acc	gtc	2058	
Val	Ile	Leu	Ala	Phe	Val	Met	Gly	Ala	Val	Phe	Ser	Gly	Ile	Thr	Val		

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Tyr Cys Val Cys Asp His Arg Arg Lys Asp Val Ala Val Val Gln Arg				
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aag gag aag gag ctc acc cac tcg cgc cgg ggc tcc atg agc agc gtc				2154
Lys Glu Lys Glu Leu Thr His Ser Arg Arg Gly Ser Met Ser Ser Val				
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acc aag ctc agc ggc ctc ttt ggg gac act caa tcc aaa gac cca aag				2202
Thr Lys Leu Ser Gly Leu Phe Gly Asp Thr Gln Ser Lys Asp Pro Lys				
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ccg gag gcc atc ctc acg cca ctc atg cac aac ggc aag ctc gcc act				2250
Pro Glu Ala Ile Leu Thr Pro Leu Met His Asn Gly Lys Leu Ala Thr				
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ccc ggc aac acg gcc aag atg ctc att aaa gca gac cag cac cac ctg				2298
Pro Gly Asn Thr Ala Lys Met Leu Ile Lys Ala Asp Gln His His Leu				
680		685	690	695
gac ctg acg gcc ctc ccc acc cca gag tca acc cca acg ctg cag cag				2346
Asp Leu Thr Ala Leu Pro Thr Pro Glu Ser Thr Pro Thr Leu Gln Gln				
700		705	710	
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Lys Arg Glu Pro Ser Arg Gly Thr Arg Glu Trp Glu Arg Asn Gln Asn				
715		720	725	
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Leu Ile Asn Ala Cys Thr Lys Asp Met Pro Pro Met Gly Ser Pro Val				
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Ile Pro Thr Asp Leu Pro Leu Arg Ala Ser Pro Ser His Ile Pro Ser				
745		750	755	
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Val Val Val Leu Pro Ile Thr Gln Gln Gly Tyr Gln His Glu Tyr Val				
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gac cag ccc aaa atg agc gag gtg gcc cag atg gcg ctg gag gac cag				2586
Asp Gln Pro Lys Met Ser Glu Val Ala Gln Met Ala Leu Glu Asp Gln				
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gcc gcc aca ctg gag tat aag acc atc aag gaa cat ctc agc agc aag				2634
Ala Ala Thr Leu Glu Tyr Lys Thr Ile Lys Glu His Leu Ser Ser Lys				
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agt ccc aac cat ggg gtg aac ctt gtg gag aac ctg gac agc ctg ccc				2682
Ser Pro Asn His Gly Val Asn Leu Val Glu Asn Leu Asp Ser Leu Pro				
810		815	820	
ccc aaa gtt cca cag cgg gag gcc tcc ctg ggt ccc ccg gga gcc tcc				2730
Pro Lys Val Pro Gln Arg Glu Ala Ser Leu Gly Pro Pro Gly Ala Ser				
825		830	835	

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 Leu Ser Gln Thr Gly Leu Ser Lys Arg Leu Glu Met His His Ser Ser
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Trp Lys Ser Arg Gln Ala Asp Val Asp Thr Cys Arg Met Lys Gly Lys
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Arg	Asn	Tyr	Lys	Met	Asp	Thr	Leu	Glu	Pro	Phe	Gly	Asp	Glu	Phe	Ser	
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Ile	Asp	Ala	Val	Ile	Tyr	Arg	Ser	Leu	Gly	Glu	Ser	Pro	Thr	Leu	Arg	
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Val	Glu	Tyr	Asn	Thr	Met	Gly	Lys	Val	Val	Phe	Pro	Arg	Val	Ala	Gln	
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Val	Cys	Lys	Asn	Asp	Met	Gly	Gly	Ser	Gln	Arg	Val	Leu	Glu	Lys	Gln	
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Pro	Asp	Asp	Thr	Leu	Asn	Phe	Ile	Lys	Thr	His	Pro	Leu	Met	Asp	Glu	
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Gln	Asn	His	Thr	Val	Val	Phe	Leu	Gly	Ser	Glu	Lys	Gly	Ile	Ile	Leu	435	440	445
Lys	Phe	Leu	Ala	Arg	Ile	Gly	Asn	Ser	Gly	Phe	Leu	Asn	Asp	Ser	Leu	450	455	460
Phe	Leu	Glu	Glu	Met	Ser	Val	Tyr	Asn	Ser	Glu	Lys	Cys	Ser	Tyr	Asp	465	470	475
Gly	Val	Glu	Asp	Lys	Arg	Ile	Met	Gly	Met	Gln	Leu	Asp	Arg	Ala	Ser	485	490	495
Ser	Ser	Leu	Tyr	Val	Ala	Phe	Ser	Thr	Cys	Val	Ile	Lys	Val	Pro	Leu	500	505	510
Gly	Arg	Cys	Glu	Arg	His	Gly	Lys	Cys	Lys	Lys	Thr	Cys	Ile	Ala	Ser	515	520	525
Arg	Asp	Pro	Tyr	Cys	Gly	Trp	Ile	Lys	Glu	Gly	Gly	Ala	Cys	Ser	His	530	535	540
Leu	Ser	Pro	Asn	Ser	Arg	Leu	Thr	Phe	Glu	Gln	Asp	Ile	Glu	Arg	Gly	545	550	555
Asn	Thr	Asp	Gly	Leu	Gly	Asp	Cys	His	Asn	Ser	Phe	Val	Ala	Leu	Asn	565	570	575
Gly	Val	Ile	Arg	Glu	Ser	Tyr	Leu	Lys	Gly	His	Asp	Gln	Leu	Val	Pro	580	585	590
Val	Thr	Leu	Leu	Ala	Ile	Ala	Val	Ile	Leu	Ala	Phe	Val	Met	Gly	Ala	595	600	605
Val	Phe	Ser	Gly	Ile	Thr	Val	Tyr	Cys	Val	Cys	Asp	His	Arg	Arg	Lys	610	615	620
Asp	Val	Ala	Val	Val	Gln	Arg	Lys	Glu	Lys	Glu	Leu	Thr	His	Ser	Arg	625	630	635
Arg	Gly	Ser	Met	Ser	Ser	Val	Thr	Lys	Leu	Ser	Gly	Leu	Phe	Gly	Asp	645	650	655
Thr	Gln	Ser	Lys	Asp	Pro	Lys	Pro	Glu	Ala	Ile	Leu	Thr	Pro	Leu	Met	660	665	670
His	Asn	Gly	Lys	Leu	Ala	Thr	Pro	Gly	Asn	Thr	Ala	Lys	Met	Leu	Ile	675	680	685
Lys	Ala	Asp	Gln	His	His	Leu	Asp	Leu	Thr	Ala	Leu	Pro	Thr	Pro	Glu	690	695	700
Ser	Thr	Pro	Thr	Leu	Gln	Gln	Lys	Arg	Glu	Pro	Ser	Arg	Gly	Thr	Arg	705	710	715
																		720

Glu	Trp	Glu	Arg	Asn	Gln	Asn	Leu	Ile	Asn	Ala	Cys	Thr	Lys	Asp	Met	
				725					730					735		
Pro	Pro	Met	Gly	Ser	Pro	Val	Ile	Pro	Thr	Asp	Leu	Pro	Leu	Arg	Ala	
			740					745					750			
Ser	Pro	Ser	His	Ile	Pro	Ser	Val	Val	Val	Leu	Pro	Ile	Thr	Gln	Gln	
		755					760					765				
Gly	Tyr	Gln	His	Glu	Tyr	Val	Asp	Gln	Pro	Lys	Met	Ser	Glu	Val	Ala	
	770					775					780					
Gln	Met	Ala	Leu	Glu	Asp	Gln	Ala	Ala	Thr	Leu	Glu	Tyr	Lys	Thr	Ile	
785					790					795					800	
Lys	Glu	His	Leu	Ser	Ser	Lys	Ser	Pro	Asn	His	Gly	Val	Asn	Leu	Val	
				805					810					815		
Glu	Asn	Leu	Asp	Ser	Leu	Pro	Pro	Lys	Val	Pro	Gln	Arg	Glu	Ala	Ser	
			820					825					830			
Leu	Gly	Pro	Pro	Gly	Ala	Ser	Leu	Ser	Gln	Thr	Gly	Leu	Ser	Lys	Arg	
		835					840					845				
Leu	Glu	Met	His	His	Ser	Ser	Ser	Tyr	Gly	Val	Asp	Tyr	Lys	Arg	Ser	
	850					855					860					
Tyr	Pro	Thr	Asn	Ser	Leu	Thr	Arg	Ser	His	Leu	Thr	Thr	Tyr	Ser	His	
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Gln	Lys	Gln	His													

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 tctgtgtttt ctctgtg atg atc atg aac att gct cag agc aat gct gtg 170
 Met Ile Met Asn Ile Ala Gln Ser Asn Ala Val
 1 5 10
 ata tca cag tgg cta ttt atg att aga tca ttt cat tgc atg ctt aca 218
 Ile Ser Gln Trp Leu Phe Met Ile Arg Ser Phe His Cys Met Leu Thr
 15 20 25

Phe Met Ile Arg Ser Phe His Cys Met Leu Thr Leu Phe Met Glu Lys
20 25 30
Cys Asn Lys Cys Gln Asn Ile Asn Gln Lys Phe Leu Leu Gln Ile Ile
35 40 45
Ala Lys Asn Leu Phe Ser Thr Pro Leu Leu Glu Tyr Ser Lys Lys Phe
50 55 60
Arg Val Ile Thr Arg Phe Gly Val Cys His Phe Trp Ala Glu Arg Asp
65 70 75 80
Phe Arg Phe Gln Arg Asn Lys Leu Cys Phe Thr Gly Ser Arg Cys Cys
85 90 95
Pro Cys Arg Phe Arg Ala Phe Arg Asn Phe Arg Cys Asn Cys Ser Gly
100 105 110
Thr Cys Gly Ser Phe Arg Phe Gly Ser Trp Arg Phe Gly Pro Gly Ala
115 120 125
Ser Phe Arg Cys Arg Arg Asp Arg Cys Ser Leu Leu Gly Ser Arg Cys
130 135 140
Arg Arg Leu His Phe Trp Thr Gly Lys Asp Phe Gln Phe Leu Arg Asn
145 150 155 160
Lys Trp Cys Phe Thr Trp Ser Gln Cys Cys Pro Trp Leu Phe Lys Ser
165 170 175
Ser Arg Ser Phe Arg Trp Asp Arg Ile Gln Asn Thr Ile Thr Cys Cys
180 185 190
Trp Val Gly Ile
195

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agaggagctc ctagctcact taagccgggg tagggctggt tctcctttcc gagccaaaat 180
cccaggcgat ggtgaattat gaacgtgccca cacc atg aag ctc ttg tgg cag gta 235
Met Lys Leu Leu Trp Gln Val

															1																5	
act	gtg	cac	cac	cac	acc	tgg	aat	gcc	atc	ctg	ctc	ccg	ttc	gtc	tac	283																
Thr	Val	His	His	His	Thr	Trp	Asn	Ala	Ile	Leu	Leu	Pro	Phe	Val	Tyr																	
		10					15					20																				
ctc	acg	gcg	caa	gtg	tgg	att	ctg	tgt	gca	gcc	atc	gct	gct	gcc	gcc	331																
Leu	Thr	Ala	Gln	Val	Trp	Ile	Leu	Cys	Ala	Ala	Ile	Ala	Ala	Ala	Ala																	
		25					30					35																				
tca	gcc	ggg	ccc	cag	aac	tgc	ccc	tcc	gtc	tgc	tcg	tgc	agt	aac	cag	379																
Ser	Ala	Gly	Pro	Gln	Asn	Cys	Pro	Ser	Val	Cys	Ser	Cys	Ser	Asn	Gln																	
		40					45					50			55																	
ttc	agc	aag	gtg	gtg	tgc	acg	cgc	cgg	ggc	ctc	tcc	gag	gtc	ccg	cag	427																
Phe	Ser	Lys	Val	Val	Cys	Thr	Arg	Arg	Gly	Leu	Ser	Glu	Val	Pro	Gln																	
		60					65					70																				
ggc	att	ccc	tcg	aac	acc	cgg	tac	ctc	aac	ctc	atg	gag	aac	aac	atc	475																
Gly	Ile	Pro	Ser	Asn	Thr	Arg	Tyr	Leu	Asn	Leu	Met	Glu	Asn	Asn	Ile																	
		75					80					85																				
cag	atg	atc	cag	gcc	gac	acc	ttc	cgc	cac	ctc	cac	cac	ctg	gag	gtc	523																
Gln	Met	Ile	Gln	Ala	Asp	Thr	Phe	Arg	His	Leu	His	His	Leu	Glu	Val																	
		90					95					100																				
ctg	cag	ttg	ggc	agg	aac	tcc	atc	cgg	cag	att	gag	gtg	ggg	gcc	ttc	571																
Leu	Gln	Leu	Gly	Arg	Asn	Ser	Ile	Arg	Gln	Ile	Glu	Val	Gly	Ala	Phe																	
		105					110					115																				
aac	ggc	ctg	gcc	agc	ctc	agc	acc	ctg	gag	ctg	ttc	gac	aac	tgg	ctg	619																
Asn	Gly	Leu	Ala	Ser	Leu	Ser	Thr	Leu	Glu	Leu	Phe	Asp	Asn	Trp	Leu																	
		120					125					130			135																	
aca	gtc	atc	cct	agc	ggg	gcc	ttt	gaa	tac	ctg	tcc	aag	ctg	cgg	gag	667																
Thr	Val	Ile	Pro	Ser	Gly	Ala	Phe	Glu	Tyr	Leu	Ser	Lys	Leu	Arg	Glu																	
		140					145					150																				
ctc	tgg	ctt	cgc	aac	aac	ccc	atc	gaa	agc	atc	ccc	tct	tac	gcc	ttc	715																
Leu	Trp	Leu	Arg	Asn	Asn	Pro	Ile	Glu	Ser	Ile	Pro	Ser	Tyr	Ala	Phe																	
		155					160					165																				
aac	cgg	gtg	ccc	tcc	ctc	atg	cgc	ctg	gac	ttg	ggg	gag	ctc	aag	aag	763																
Asn	Arg	Val	Pro	Ser	Leu	Met	Arg	Leu	Asp	Leu	Gly	Glu	Leu	Lys	Lys																	
		170					175					180																				
ctg	gag	tat	atc	tct	gag	gga	gct	ttt	gag	ggg	ctg	ttc	aac	ctc	aag	811																
Leu	Glu	Tyr	Ile	Ser	Glu	Gly	Ala	Phe	Glu	Gly	Leu	Phe	Asn	Leu	Lys																	
		185					190					195																				
tat	ctg	aac	ttg	ggc	atg	tgc	aac	att	aaa	gac	atg	ccc	aat	ctc	acc	859																
Tyr	Leu	Asn	Leu	Gly	Met	Cys	Asn	Ile	Lys	Asp	Met	Pro	Asn	Leu	Thr																	
		200					205					210			215																	
ccc	ctg	gtg	ggg	ctg	gag	gag	ctg	gag	atg	tca	ggg	aac	cac	ttc	cct	907																
Pro	Leu	Val	Gly	Leu	Glu	Glu	Leu	Glu	Met	Ser	Gly	Asn	His	Phe	Pro																	
		220					225					230																				

gag atc agg cct ggc tcc ttc cat ggc ctg agc tcc ctc aag aag ctc	955
Glu Ile Arg Pro Gly Ser Phe His Gly Leu Ser Ser Leu Lys Lys Leu	
235 240 245	
tgg gtc atg aac tca cag gtc agc ctg att gag cgg aat gct ttt gac	1003
Trp Val Met Asn Ser Gln Val Ser Leu Ile Glu Arg Asn Ala Phe Asp	
250 255 260	
ggg ctg gct tca ctt gtg gaa ctc aac ttg gcc cac aat aac ctc tct	1051
Gly Leu Ala Ser Leu Val Glu Leu Asn Leu Ala His Asn Asn Leu Ser	
265 270 275	
tct ttg ccc cat gac ctc ttt acc ccg ctg agg tac ctg gtg gag ttg	1099
Ser Leu Pro His Asp Leu Phe Thr Pro Leu Arg Tyr Leu Val Glu Leu	
280 285 290 295	
cat cta cac cac aac cct tgg aac tgt gat tgt gac att ctg tgg cta	1147
His Leu His His Asn Pro Trp Asn Cys Asp Cys Asp Ile Leu Trp Leu	
300 305 310	
gcc tgg tgg ctt cga gag tat ata ccc acc aat tcc acc tgc tgt ggc	1195
Ala Trp Trp Leu Arg Glu Tyr Ile Pro Thr Asn Ser Thr Cys Cys Gly	
315 320 325	
cgc tgt cat gct ccc atg cac atg cga ggc cgc tac ctc gtg gag gtg	1243
Arg Cys His Ala Pro Met His Met Arg Gly Arg Tyr Leu Val Glu Val	
330 335 340	
gac cag gcc tcc ttc cag tgc tct gcc ccc ttc atc atg gac gca cct	1291
Asp Gln Ala Ser Phe Gln Cys Ser Ala Pro Phe Ile Met Asp Ala Pro	
345 350 355	
cga gac ctc aac att tct gag ggt cgg atg gca gaa ctt aag tgt cgg	1339
Arg Asp Leu Asn Ile Ser Glu Gly Arg Met Ala Glu Leu Lys Cys Arg	
360 365 370 375	
act ccc cct atg tcc tcc gtg aag tgg ttg ctg ccc aat ggg aca gtg	1387
Thr Pro Pro Met Ser Ser Val Lys Trp Leu Leu Pro Asn Gly Thr Val	
380 385 390	
ctc agc cac gcc tcc cgc cac cca agg atc tct gtc ctc aac gac ggc	1435
Leu Ser His Ala Ser Arg His Pro Arg Ile Ser Val Leu Asn Asp Gly	
395 400 405	
acc ttg aac ttt tcc cac gtg ctg ctt tca gac act ggg gtg tac aca	1483
Thr Leu Asn Phe Ser His Val Leu Leu Ser Asp Thr Gly Val Tyr Thr	
410 415 420	
tgc atg ggg acc aat gtt gca ggc aac tcc aac gcc tcg gcc tac ctc	1531
Cys Met Gly Thr Asn Val Ala Gly Asn Ser Asn Ala Ser Ala Tyr Leu	
425 430 435	
aat ggg agc acg gct gag ctt aac acc tcc aac tac agc ttc ttc acc	1579
Asn Gly Ser Thr Ala Glu Leu Asn Thr Ser Asn Tyr Ser Phe Phe Thr	
440 445 450 455	

aca gga aca ggg gag acc acg gag atc tcg cct gag gac aca acg cga	1627
Thr Gly Thr Gly Glu Thr Thr Glu Ile Ser Pro Glu Asp Thr Thr Arg	
460 465 470	
aag tac aag cct gtt cct acc acg tcc act ggt tac cag ccg gca tat	1675
Lys Tyr Lys Pro Val Pro Thr Thr Ser Thr Gly Tyr Gln Pro Ala Tyr	
475 480 485	
acc acc tct acc acg gtg ctc att cag act acc cgt gtg ccc aag cag	1723
Thr Thr Ser Thr Thr Val Leu Ile Gln Thr Thr Arg Val Pro Lys Gln	
490 495 500	
gtg gca gta ccc gcg aca gac acc act gac aag atg cag acc agc ctg	1771
Val Ala Val Pro Ala Thr Asp Thr Thr Asp Lys Met Gln Thr Ser Leu	
505 510 515	
gat gaa gtc atg aag acc acc aag atc atc att ggc tgc ttt gtg gca	1819
Asp Glu Val Met Lys Thr Thr Lys Ile Ile Ile Gly Cys Phe Val Ala	
520 525 530 535	
gtg act ctg cta gct gcc gcc atg ttg att gtc ttc tat aaa ctt cgt	1867
Val Thr Leu Leu Ala Ala Ala Met Leu Ile Val Phe Tyr Lys Leu Arg	
540 545 550	
aag cgg cac cag cag cgg agt aca gtc aca gcc gcc cgg act gtt gag	1915
Lys Arg His Gln Gln Arg Ser Thr Val Thr Ala Ala Arg Thr Val Glu	
555 560 565	
ata atc cag gtg gac gaa gac atc cca gca gca aca tcc gca gca gca	1963
Ile Ile Gln Val Asp Glu Asp Ile Pro Ala Ala Thr Ser Ala Ala Ala	
570 575 580	
aca gca gct ccg tcc ggt gta tca ggt gaa ggg gca gta gtg ctg ccc	2011
Thr Ala Ala Pro Ser Gly Val Ser Gly Glu Gly Ala Val Val Leu Pro	
585 590 595	
aca att cat gac cat att aac tac aac acc tac aaa cca gca cat ggg	2059
Thr Ile His Asp His Ile Asn Tyr Asn Thr Tyr Lys Pro Ala His Gly	
600 605 610 615	
gcc cac tgg aca gaa aac agc ctg ggg aac tct ctg cac ccc aca gtc	2107
Ala His Trp Thr Glu Asn Ser Leu Gly Asn Ser Leu His Pro Thr Val	
620 625 630	
acc act atc tct gaa cct tat ata att cag acc cat acc aag gac aag	2155
Thr Thr Ile Ser Glu Pro Tyr Ile Ile Gln Thr His Thr Lys Asp Lys	
635 640 645	
gta cag gaa act caa ata tgactcccct cccccaaaaa acttataaaa	2203
Val Gln Glu Thr Gln Ile	
650	
tgcaatagaa tgcacacaaa gacagcaact tttgtacaga gtggggagag acttttttctt	2263
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Ile Leu Leu Pro Phe Val Tyr Leu Thr Ala Gln Val Trp Ile Leu Cys
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Ala Ala Ile Ala Ala Ala Ala Ser Ala Gly Pro Gln Asn Cys Pro Ser
 35 40 45

Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val Val Cys Thr Arg Arg
 50 55 60

Gly Leu Ser Glu Val Pro Gln Gly Ile Pro Ser Asn Thr Arg Tyr Leu
 65 70 75 80

Asn Leu Met Glu Asn Asn Ile Gln Met Ile Gln Ala Asp Thr Phe Arg
 85 90 95

His Leu His His Leu Glu Val Leu Gln Leu Gly Arg Asn Ser Ile Arg
 100 105 110

Gln Ile Glu Val Gly Ala Phe Asn Gly Leu Ala Ser Leu Ser Thr Leu
 115 120 125

Glu Leu Phe Asp Asn Trp Leu Thr Val Ile Pro Ser Gly Ala Phe Glu
 130 135 140

Tyr Leu Ser Lys Leu Arg Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu
 145 150 155 160

Ser Ile Pro Ser Tyr Ala Phe Asn Arg Val Pro Ser Leu Met Arg Leu
 165 170 175

Asp Leu Gly Glu Leu Lys Lys Leu Glu Tyr Ile Ser Glu Gly Ala Phe
 180 185 190

Glu Gly Leu Phe Asn Leu Lys Tyr Leu Asn Leu Gly Met Cys Asn Ile
 195 200 205

Lys Asp Met Pro Asn Leu Thr Pro Leu Val Gly Leu Glu Glu Leu Glu
 210 215 220

Met Ser Gly Asn His Phe Pro Glu Ile Arg Pro Gly Ser Phe His Gly
 225 230 235 240

Leu Ser Ser Leu Lys Lys Leu Trp Val Met Asn Ser Gln Val Ser Leu
 245 250 255

Ile Glu Arg Asn Ala Phe Asp Gly Leu Ala Ser Leu Val Glu Leu Asn

260					265					270					
Leu	Ala	His	Asn	Asn	Leu	Ser	Ser	Leu	Pro	His	Asp	Leu	Phe	Thr	Pro
		275					280					285			
Leu	Arg	Tyr	Leu	Val	Glu	Leu	His	Leu	His	His	Asn	Pro	Trp	Asn	Cys
	290					295					300				
Asp	Cys	Asp	Ile	Leu	Trp	Leu	Ala	Trp	Trp	Leu	Arg	Glu	Tyr	Ile	Pro
305					310					315					320
Thr	Asn	Ser	Thr	Cys	Cys	Gly	Arg	Cys	His	Ala	Pro	Met	His	Met	Arg
				325					330					335	
Gly	Arg	Tyr	Leu	Val	Glu	Val	Asp	Gln	Ala	Ser	Phe	Gln	Cys	Ser	Ala
			340					345					350		
Pro	Phe	Ile	Met	Asp	Ala	Pro	Arg	Asp	Leu	Asn	Ile	Ser	Glu	Gly	Arg
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Met	Ala	Glu	Leu	Lys	Cys	Arg	Thr	Pro	Pro	Met	Ser	Ser	Val	Lys	Trp
	370					375					380				
Leu	Leu	Pro	Asn	Gly	Thr	Val	Leu	Ser	His	Ala	Ser	Arg	His	Pro	Arg
385					390					395					400
Ile	Ser	Val	Leu	Asn	Asp	Gly	Thr	Leu	Asn	Phe	Ser	His	Val	Leu	Leu
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Ser	Asp	Thr	Gly	Val	Tyr	Thr	Cys	Met	Gly	Thr	Asn	Val	Ala	Gly	Asn
			420					425					430		
Ser	Asn	Ala	Ser	Ala	Tyr	Leu	Asn	Gly	Ser	Thr	Ala	Glu	Leu	Asn	Thr
		435					440					445			
Ser	Asn	Tyr	Ser	Phe	Phe	Thr	Thr	Gly	Thr	Gly	Glu	Thr	Thr	Glu	Ile
	450					455					460				
Ser	Pro	Glu	Asp	Thr	Thr	Arg	Lys	Tyr	Lys	Pro	Val	Pro	Thr	Thr	Ser
465					470					475					480
Thr	Gly	Tyr	Gln	Pro	Ala	Tyr	Thr	Thr	Ser	Thr	Thr	Val	Leu	Ile	Gln
				485					490					495	
Thr	Thr	Arg	Val	Pro	Lys	Gln	Val	Ala	Val	Pro	Ala	Thr	Asp	Thr	Thr
			500					505					510		
Asp	Lys	Met	Gln	Thr	Ser	Leu	Asp	Glu	Val	Met	Lys	Thr	Thr	Lys	Ile
		515					520					525			
Ile	Ile	Gly	Cys	Phe	Val	Ala	Val	Thr	Leu	Leu	Ala	Ala	Ala	Met	Leu
	530					535					540				
Ile	Val	Phe	Tyr	Lys	Leu	Arg	Lys	Arg	His	Gln	Gln	Arg	Ser	Thr	Val
545					550					555					560
Thr	Ala	Ala	Arg	Thr	Val	Glu	Ile	Ile	Gln	Val	Asp	Glu	Asp	Ile	Pro

565										570					575				
Ala	Ala	Thr	Ser	Ala	Ala	Ala	Thr	Ala	Ala	Pro	Ser	Gly	Val	Ser	Gly				
			580					585					590						
Glu	Gly	Ala	Val	Val	Leu	Pro	Thr	Ile	His	Asp	His	Ile	Asn	Tyr	Asn				
		595					600					605							
Thr	Tyr	Lys	Pro	Ala	His	Gly	Ala	His	Trp	Thr	Glu	Asn	Ser	Leu	Gly				
	610					615					620								
Asn	Ser	Leu	His	Pro	Thr	Val	Thr	Thr	Ile	Ser	Glu	Pro	Tyr	Ile	Ile				
625					630					635					640				
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 agaggagctc ctagctcact taagccgggg tagggctggt tctcctttcc gagccaaaat 180
 cccaggcgat ggtgaattat gaacgtgccca cacc atg aag ctc ttg tgg cag gta 235
 Met Lys Leu Leu Trp Gln Val
 1 5
 act gtg cac cac cac acc tgg aat gcc atc ctg ctc ccg ttc gtc tac 283
 Thr Val His His His Thr Trp Asn Ala Ile Leu Leu Pro Phe Val Tyr
 10 15 20
 ctc acg gcg caa gtg tgg att ctg tgt gca gcc atc gct gct gcc gcc 331
 Leu Thr Ala Gln Val Trp Ile Leu Cys Ala Ala Ile Ala Ala Ala Ala
 25 30 35
 tca gcc ggg ccc cag aac tgc ccc tcc gtc tgc tcg tgc agt aac cag 379
 Ser Ala Gly Pro Gln Asn Cys Pro Ser Val Cys Ser Cys Ser Asn Gln
 40 45 50 55
 ttc agc aag gtg gtg tgc acg cgc cgg ggc ctc tcc gag gtc ccg cag 427
 Phe Ser Lys Val Val Cys Thr Arg Arg Gly Leu Ser Glu Val Pro Gln
 60 65 70
 ggt att ccc tcg aac acc cgg tac ctc aac ctc atg gag aac aac atc 475
 Gly Ile Pro Ser Asn Thr Arg Tyr Leu Asn Leu Met Glu Asn Asn Ile

75	80	85	
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ctg cag ttg ggc agg aac tcc atc cgg cag att gag gtg ggg gcc ttc Leu Gln Leu Gly Arg Asn Ser Ile Arg Gln Ile Glu Val Gly Ala Phe 105 110 115			571
aac ggc ctg gcc agc ctc agc acc ctg gag ctg ttc gac aac tgg ctg Asn Gly Leu Ala Ser Leu Ser Thr Leu Glu Leu Phe Asp Asn Trp Leu 120 125 130 135			619
aca gtc atc cct agc ggg gcc ttt gaa tac ctg tcc aag ctg cgg gag Thr Val Ile Pro Ser Gly Ala Phe Glu Tyr Leu Ser Lys Leu Arg Glu 140 145 150			667
ctc tgg ctt cgc aac aac ccc atc gaa agc atc ccc tct tac gcc ttc Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser Tyr Ala Phe 155 160 165			715
aac cgg gtg ccc tcc ctc atg cgc ctg gac ttg ggg gag ctc aag aag Asn Arg Val Pro Ser Leu Met Arg Leu Asp Leu Gly Glu Leu Lys Lys 170 175 180			763
ctg gag tat atc tct gag gga gct ttt gag ggg ctg ttc aac ctc aag Leu Glu Tyr Ile Ser Glu Gly Ala Phe Glu Gly Leu Phe Asn Leu Lys 185 190 195			811
tat ctg aac ttg ggc atg tgc aac att aaa gac atg ccc aat ctc acc Tyr Leu Asn Leu Gly Met Cys Asn Ile Lys Asp Met Pro Asn Leu Thr 200 205 210 215			859
ccc ctg gtg ggg ctg gag gag ctg gag atg tca ggg aac cac ttc cct Pro Leu Val Gly Leu Glu Glu Leu Glu Met Ser Gly Asn His Phe Pro 220 225 230			907
gag atc agg cct ggc tcc ttc cat ggc ctg agc tcc ctc aag aag ctc Glu Ile Arg Pro Gly Ser Phe His Gly Leu Ser Ser Leu Lys Lys Leu 235 240 245			955
tgg gtc atg aac tca cag gtc agc ctg att gag cgg aat gct ttt gac Trp Val Met Asn Ser Gln Val Ser Leu Ile Glu Arg Asn Ala Phe Asp 250 255 260			1003
ggg ctg gct tca ctt gtg gaa ctc aac ttg gcc cac aat aac ctc tct Gly Leu Ala Ser Leu Val Glu Leu Asn Leu Ala His Asn Asn Leu Ser 265 270 275			1051
tct ttg ccc cat gac ctc ttt acc ccg ctg agg tac ctg gtg gag ttg Ser Leu Pro His Asp Leu Phe Thr Pro Leu Arg Tyr Leu Val Glu Leu 280 285 290 295			1099
cat cta cac cac aac cct tgg aac tgt gat tgt gac att ctg tgg cta His Leu His His Asn Pro Trp Asn Cys Asp Cys Asp Ile Leu Trp Leu 300 305 310			1147

gcc tgg tgg ctt cga gag tat ata ccc acc aat tcc acc tgc tgt ggc	1195
Ala Trp Trp Leu Arg Glu Tyr Ile Pro Thr Asn Ser Thr Cys Cys Gly	
315 320 325	
cgc tgt cat gct ccc atg cac atg cga ggc cgc tac ctc gtg gag gtg	1243
Arg Cys His Ala Pro Met His Met Arg Gly Arg Tyr Leu Val Glu Val	
330 335 340	
gac cag gcc tcc ttc cag tgc tct gcc ccc ttc atc atg gac gca cct	1291
Asp Gln Ala Ser Phe Gln Cys Ser Ala Pro Phe Ile Met Asp Ala Pro	
345 350 355	
cga gac ctc aac att tct gag ggt cgg atg gca gaa ctt aag tgt cgg	1339
Arg Asp Leu Asn Ile Ser Glu Gly Arg Met Ala Glu Leu Lys Cys Arg	
360 365 370 375	
act ccc cct atg tcc tcc gtg aag tgg ttg ctg ccc aat ggg aca gtg	1387
Thr Pro Pro Met Ser Ser Val Lys Trp Leu Leu Pro Asn Gly Thr Val	
380 385 390	
ctc agc cac gcc tcc cgc cac cca agg atc tct gtc ctc aac gac ggc	1435
Leu Ser His Ala Ser Arg His Pro Arg Ile Ser Val Leu Asn Asp Gly	
395 400 405	
acc ttg aac ttt tcc cac gtg ctg ctt tca gac act ggg gtg tac aca	1483
Thr Leu Asn Phe Ser His Val Leu Leu Ser Asp Thr Gly Val Tyr Thr	
410 415 420	
tgc atg ggg acc aat gtt gca ggc aac tcc aac gcc tcg gcc tac ctc	1531
Cys Met Gly Thr Asn Val Ala Gly Asn Ser Asn Ala Ser Ala Tyr Leu	
425 430 435	
aat ggg agc acg gct gag ctt aac acc tcc aac tac agc ttc ttc acc	1579
Asn Gly Ser Thr Ala Glu Leu Asn Thr Ser Asn Tyr Ser Phe Phe Thr	
440 445 450 455	
aca gga aca ggg gag acc acg gag atc tcg cct gag gac aca acg cga	1627
Thr Gly Thr Gly Glu Thr Thr Glu Ile Ser Pro Glu Asp Thr Thr Arg	
460 465 470	
aag tac aag cct gtt cct acc acg tcc act ggt tac cag ccg gca tat	1675
Lys Tyr Lys Pro Val Pro Thr Thr Ser Thr Gly Tyr Gln Pro Ala Tyr	
475 480 485	
acc acc tct acc acg gtg ctc att cag act acc cgt gtg ccc aag cag	1723
Thr Thr Ser Thr Thr Val Leu Ile Gln Thr Thr Arg Val Pro Lys Gln	
490 495 500	
gtg gca gta ccc gcg aca gac acc act gac aag atg cag acc agc ctg	1771
Val Ala Val Pro Ala Thr Asp Thr Thr Asp Lys Met Gln Thr Ser Leu	
505 510 515	
gat gaa gtc atg aag acc acc aag atc atc att ggc tgc ttt gtg gca	1819
Asp Glu Val Met Lys Thr Thr Lys Ile Ile Ile Gly Cys Phe Val Ala	
520 525 530 535	

gtg act ctg cta gct gcc gcc atg ttg att gtc ttc tat aaa ctt cgt 1867
Val Thr Leu Leu Ala Ala Ala Met Leu Ile Val Phe Tyr Lys Leu Arg
540 545 550

aag cgg cac cag cag cgg agt aca gtc aca gcc gcc ccc aca ctg gag 1915
Lys Arg His Gln Gln Arg Ser Thr Val Thr Ala Ala Pro Thr Leu Glu
555 560 565

aga aaa cac agg gac aaa aac aca cca caa caa aaa cac cca caa caa 1963
Arg Lys His Arg Asp Lys Asn Thr Pro Gln Gln Lys His Pro Gln Gln
570 575 580

aaa caa cag ccc ccc ccg gta taacaggaaa gggcacaata gcgccccaca 2014
Lys Gln Gln Pro Pro Pro Val
585 590

aaacacaaca acataaaaaa caaaacacac acaaaccagc acatggggcc cactggacag 2074

aaaacagcct ggggaactct gtgcacccca cagtcaccac tatctctgaa ccttatataa 2134

ttcagaccca taccaaggac aaggtacagg aaactcaa atgactcccc tcccccaaaa 2194

aacttataaa atgcaataga atgcacacaa agacagcaac ttttgtacag agtggggaga 2254

gacttttttct tgtatatgct tatatatataa gtctatgggc tggttaaaaa aaacagatta 2314

tattaaaatt taaagacaaa aagtcaaaac aaaaatatatt tctaacttgt aaatttctatt 2374

taaaggggggt ggggggggaat cttgggaacg ttgtggggta caagccacaa gttaacttgc 2434

tatgctgccga gaagggattt ctggtataag gttgaaattg ctgagataaa ataaactaaa 2494

acaacaaaca tccttaaaga ggtaggggtgt gggctgctga aggggcaaga gggatagact 2554

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<211> 590

<212> PRT

<213> Homo sapiens

<400> 12

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1 5 10 15

Ile Leu Leu Pro Phe Val Tyr Leu Thr Ala Gln Val Trp Ile Leu Cys
20 25 30

Ala Ala Ile Ala Ala Ala Ala Ser Ala Gly Pro Gln Asn Cys Pro Ser
35 40 45

Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val Val Cys Thr Arg Arg
50 55 60

Gly Leu Ser Glu Val Pro Gln Gly Ile Pro Ser Asn Thr Arg Tyr Leu
65 70 75 80

Asn	Leu	Met	Glu	Asn	Asn	Ile	Gln	Met	Ile	Gln	Ala	Asp	Thr	Phe	Arg	85	90	95
His	Leu	His	His	Leu	Glu	Val	Leu	Gln	Leu	Gly	Arg	Asn	Ser	Ile	Arg	100	105	110
Gln	Ile	Glu	Val	Gly	Ala	Phe	Asn	Gly	Leu	Ala	Ser	Leu	Ser	Thr	Leu	115	120	125
Glu	Leu	Phe	Asp	Asn	Trp	Leu	Thr	Val	Ile	Pro	Ser	Gly	Ala	Phe	Glu	130	135	140
Tyr	Leu	Ser	Lys	Leu	Arg	Glu	Leu	Trp	Leu	Arg	Asn	Asn	Pro	Ile	Glu	145	150	155
Ser	Ile	Pro	Ser	Tyr	Ala	Phe	Asn	Arg	Val	Pro	Ser	Leu	Met	Arg	Leu	165	170	175
Asp	Leu	Gly	Glu	Leu	Lys	Lys	Leu	Glu	Tyr	Ile	Ser	Glu	Gly	Ala	Phe	180	185	190
Glu	Gly	Leu	Phe	Asn	Leu	Lys	Tyr	Leu	Asn	Leu	Gly	Met	Cys	Asn	Ile	195	200	205
Lys	Asp	Met	Pro	Asn	Leu	Thr	Pro	Leu	Val	Gly	Leu	Glu	Glu	Leu	Glu	210	215	220
Met	Ser	Gly	Asn	His	Phe	Pro	Glu	Ile	Arg	Pro	Gly	Ser	Phe	His	Gly	225	230	235
Leu	Ser	Ser	Leu	Lys	Lys	Leu	Trp	Val	Met	Asn	Ser	Gln	Val	Ser	Leu	245	250	255
Ile	Glu	Arg	Asn	Ala	Phe	Asp	Gly	Leu	Ala	Ser	Leu	Val	Glu	Leu	Asn	260	265	270
Leu	Ala	His	Asn	Asn	Leu	Ser	Ser	Leu	Pro	His	Asp	Leu	Phe	Thr	Pro	275	280	285
Leu	Arg	Tyr	Leu	Val	Glu	Leu	His	Leu	His	His	Asn	Pro	Trp	Asn	Cys	290	295	300
Asp	Cys	Asp	Ile	Leu	Trp	Leu	Ala	Trp	Trp	Leu	Arg	Glu	Tyr	Ile	Pro	305	310	315
Thr	Asn	Ser	Thr	Cys	Cys	Gly	Arg	Cys	His	Ala	Pro	Met	His	Met	Arg	325	330	335
Gly	Arg	Tyr	Leu	Val	Glu	Val	Asp	Gln	Ala	Ser	Phe	Gln	Cys	Ser	Ala	340	345	350
Pro	Phe	Ile	Met	Asp	Ala	Pro	Arg	Asp	Leu	Asn	Ile	Ser	Glu	Gly	Arg	355	360	365
Met	Ala	Glu	Leu	Lys	Cys	Arg	Thr	Pro	Pro	Met	Ser	Ser	Val	Lys	Trp	370	375	380

Leu Leu Pro Asn Gly Thr Val Leu Ser His Ala Ser Arg His Pro Arg
 385 390 395 400
 Ile Ser Val Leu Asn Asp Gly Thr Leu Asn Phe Ser His Val Leu Leu
 405 410 415
 Ser Asp Thr Gly Val Tyr Thr Cys Met Gly Thr Asn Val Ala Gly Asn
 420 425 430
 Ser Asn Ala Ser Ala Tyr Leu Asn Gly Ser Thr Ala Glu Leu Asn Thr
 435 440 445
 Ser Asn Tyr Ser Phe Phe Thr Thr Gly Thr Gly Glu Thr Thr Glu Ile
 450 455 460
 Ser Pro Glu Asp Thr Thr Arg Lys Tyr Lys Pro Val Pro Thr Thr Ser
 465 470 475 480
 Thr Gly Tyr Gln Pro Ala Tyr Thr Thr Ser Thr Thr Val Leu Ile Gln
 485 490 495
 Thr Thr Arg Val Pro Lys Gln Val Ala Val Pro Ala Thr Asp Thr Thr
 500 505 510
 Asp Lys Met Gln Thr Ser Leu Asp Glu Val Met Lys Thr Thr Lys Ile
 515 520 525
 Ile Ile Gly Cys Phe Val Ala Val Thr Leu Leu Ala Ala Ala Met Leu
 530 535 540
 Ile Val Phe Tyr Lys Leu Arg Lys Arg His Gln Gln Arg Ser Thr Val
 545 550 555 560
 Thr Ala Ala Pro Thr Leu Glu Arg Lys His Arg Asp Lys Asn Thr Pro
 565 570 575
 Gln Gln Lys His Pro Gln Gln Lys Gln Gln Pro Pro Pro Val
 580 585 590

<210> 13

<211> 1340

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (421)..(1287)

<220>

<221> misc_feature

<222> (22)

<223> an n may be any one of a or t or g or c

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 agccagtggg catggaatgg gctgggggtca aagactgggt gcctgggagc tgaggcagcc 120
 accgtttcag cctggccagc cctctggacc ccgaggttgg accctactgt gacacaccta 180
 ccatgcggac actcttcaac ctctctggc ttgcctggc ctgcagccct gttcacacta 240
 ccctgtcaaa gtcagatgcc aaaaaagccg cctcaaagac gctgctggag aagagtcagt 300
 ttccagataa gccggtgcaa gaccgggggtt tgggtggtgac ggacctcaaa gctgagagtg 360
 tggttcttga gcatcgagc tactgctcgg caaaggcccg ggacagacac tttgctgggg 420

 atg tac tgg gct atg tca ctc cac cag tgg aac agc cat ggc tac gat 468
 Met Tyr Trp Ala Met Ser Leu His Gln Trp Asn Ser His Gly Tyr Asp
 1 5 10 15

 gtc acc aag gtc ttt ggg agc aag ttc aca cag atc tca ccc gtc tgg 516
 Val Thr Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val Trp
 20 25 30

 ctg cag ctg aag aga cgt ggc cgt gag atg ttt gag gtc acg ggc ctc 564
 Leu Gln Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr Gly Leu
 35 40 45

 cac gac gtg gac caa ggg tgg atg cga gct gtc agg aag cat gcc aag 612
 His Asp Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys
 50 55 60

 ggc ctg cac ata gtg cct cgg ctc ctg ttt gag gac tgg act tac gat 660
 Gly Leu His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr Asp
 65 70 75 80

 gat ttc cgg aac gtc tta gac agt gag gat gag ata gag gag ctg agc 708
 Asp Phe Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu Ser
 85 90 95

 aag acc gtg gtc cag gtg gca aag aac cag cat ttc gat ggc ttc gtg 756
 Lys Thr Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe Val
 100 105 110

 gtg gag gtc tgg aac cag ctg cta agc cag aag cgc gtg ggc ctc atc 804
 Val Glu Val Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly Leu Ile
 115 120 125

 cac atg ctc acc cac ttg gcc gag gct ctg cac cag gcc cgg ctg ctg 852
 His Met Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg Leu Leu
 130 135 140

 gcc ctc ctg gtc atc ccg cct gcc atc acc ccc ggg acc gac cag ctg 900
 Ala Leu Leu Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp Gln Leu
 145 150 155 160

 ggc atg ttc acg cac aag gag ttt gag cag ctg gcc ccc gtg ctg gat 948
 Gly Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val Leu Asp
 165 170 175

ggt ttc agc ctc atg acc tac gac tac tct aca gcg cat cag cct ggc 996
 Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala His Gln Pro Gly
 180 185 190

cct aat gca ccc ctg tcc tgg gtt cga gcc tgc gtc cag gtc ctg gac 1044
 Pro Asn Ala Pro Leu Ser Trp Val Arg Ala Cys Val Gln Val Leu Asp
 195 200 205

ccg aag tcc aag tgg cga agc aaa atc ctc ctg ggg ctc aac ttc tat 1092
 Pro Lys Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly Leu Asn Phe Tyr
 210 215 220

ggt atg gac tac gcg acc tcc aag gat gcc cgt gag cct gtt gtc ggg 1140
 Gly Met Asp Tyr Ala Thr Ser Lys Asp Ala Arg Glu Pro Val Val Gly
 225 230 235 240

gcc agg tac atg cag aca ctg aag tct gca ttc gta ctc tta gca aac 1188
 Ala Arg Tyr Met Gln Thr Leu Lys Ser Ala Phe Val Leu Leu Ala Asn
 245 250 255

ttg gaa aat ttg agg cga aat tct tca aat aaa aaa aaa aaa aaa aaa 1236
 Leu Glu Asn Leu Arg Arg Asn Ser Ser Asn Lys Lys Lys Lys Lys Lys
 260 265 270

aat ttt ttc tgt ttc ttc tct tct gtc ttc tcg ttt gga gac cac aaa 1284
 Asn Phe Phe Cys Phe Phe Ser Ser Val Phe Ser Phe Gly Asp His Lys
 275 280 285

cac tagatccatt gaatttgtcc cacagctcac gaatacacct tttacctttt gga 1340
 His

<210> 14
 <211> 289
 <212> PRT
 <213> Homo sapiens

<400> 14
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Val Thr Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val Trp
 20 25 30

Leu Gln Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr Gly Leu
 35 40 45

His Asp Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys
 50 55 60

Gly Leu His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr Asp
 65 70 75 80

Asp Phe Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu Ser
 85 90 95

Lys Thr Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe Val
 100 105 110
 Val Glu Val Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly Leu Ile
 115 120 125
 His Met Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg Leu Leu
 130 135 140
 Ala Leu Leu Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp Gln Leu
 145 150 155 160
 Gly Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val Leu Asp
 165 170 175
 Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala His Gln Pro Gly
 180 185 190
 Pro Asn Ala Pro Leu Ser Trp Val Arg Ala Cys Val Gln Val Leu Asp
 195 200 205
 Pro Lys Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly Leu Asn Phe Tyr
 210 215 220
 Gly Met Asp Tyr Ala Thr Ser Lys Asp Ala Arg Glu Pro Val Val Gly
 225 230 235 240
 Ala Arg Tyr Met Gln Thr Leu Lys Ser Ala Phe Val Leu Leu Ala Asn
 245 250 255
 Leu Glu Asn Leu Arg Arg Asn Ser Ser Asn Lys Lys Lys Lys Lys Lys
 260 265 270
 Asn Phe Phe Cys Phe Phe Ser Ser Val Phe Ser Phe Gly Asp His Lys
 275 280 285

His

<210> 15
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 <212> DNA
 <213> Homo sapiens

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 <222> (96)..(905)

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tgccgccgcc gcgcgcggat tctgcttctc agaag atg cac tat tat aga tac 113
 Met His Tyr Tyr Arg Tyr

tct aac gcc aag gtc agc tgc tgg tac aag tac ctc ctt ttc agc tac	161
Ser Asn Ala Lys Val Ser Cys Trp Tyr Lys Tyr Leu Leu Phe Ser Tyr	
10 15 20	
aac atc atc ttc tgg ttg gct gga gtt gtc ttc ctt gga gtc ggg ttg	209
Asn Ile Ile Phe Trp Leu Ala Gly Val Val Phe Leu Gly Val Gly Leu	
25 30 35	
tgg gca tgg agc gaa aag ggt gtg ctg tcc gac ctc acc aaa gtg acc	257
Trp Ala Trp Ser Glu Lys Gly Val Leu Ser Asp Leu Thr Lys Val Thr	
40 45 50	
cgg atg cat gga atc gac cct gcg gtg ctg gtc ctg atg gtg ggc gcg	305
Arg Met His Gly Ile Asp Pro Ala Val Leu Val Leu Met Val Gly Ala	
55 60 65 70	
gtg atg ttc acc ctg ggg ttc gcc ggc cgc gtg ggg gcg cgc agg gag	353
Val Met Phe Thr Leu Gly Phe Ala Gly Arg Val Gly Ala Arg Arg Glu	
75 80 85	
aat atc tgc ttg ctc aac ttt ttc tgt ggc acc atc gtg ctc atc ttc	401
Asn Ile Cys Leu Leu Asn Phe Phe Cys Gly Thr Ile Val Leu Ile Phe	
90 95 100	
ttc ctg gag ctg gct gtg gcc gtg ctg gcc ttc ctg ttc cag gac tgg	449
Phe Leu Glu Leu Ala Val Ala Val Leu Ala Phe Leu Phe Gln Asp Trp	
105 110 115	
gtg agg gac cgg ttc cgg gag ttc ttc gag agc aac atc aag tcc tac	497
Val Arg Asp Arg Phe Arg Glu Phe Phe Glu Ser Asn Ile Lys Ser Tyr	
120 125 130	
cgg gac gat atc gat ctg caa aac ctc atc gac tcc ctt cag aaa gct	545
Arg Asp Asp Ile Asp Leu Gln Asn Leu Ile Asp Ser Leu Gln Lys Ala	
135 140 145 150	
aac cag tgc tgt ggc gca tat ggc cct gaa gac tgg gac ctc aac gtc	593
Asn Gln Cys Cys Gly Ala Tyr Gly Pro Glu Asp Trp Asp Leu Asn Val	
155 160 165	
tac ttc aat tgc agc ggt gcc agc tac agc cga gag aag tgc ggg gtc	641
Tyr Phe Asn Cys Ser Gly Ala Ser Tyr Ser Arg Glu Lys Cys Gly Val	
170 175 180	
ccc ttc tcc tgc tgc gtg cca gat cct gcg caa aaa gtt gtg aac aca	689
Pro Phe Ser Cys Cys Val Pro Asp Pro Ala Gln Lys Val Val Asn Thr	
185 190 195	
cag tgt gga tat gat gtc agg att cag ctg aag agc aag tgg gat gag	737
Gln Cys Gly Tyr Asp Val Arg Ile Gln Leu Lys Ser Lys Trp Asp Glu	
200 205 210	
tcc atc ttc acg aaa ggc tgc atc cag gcg ctg gaa agc tgg ctc ccg	785
Ser Ile Phe Thr Lys Gly Cys Ile Gln Ala Leu Glu Ser Trp Leu Pro	
215 220 225 230	
cgg aac att tac att gtg gct ggc gtc ttc atc gcc atc tcg ctg ttg	833

Arg Asn Ile Tyr Ile Val Ala Gly Val Phe Ile Ala Ile Ser Leu Leu
235 240 245

cag ata ttt ggc atc ttc ctg gca agg acg ctg atc tca gac atc gag 881
Gln Ile Phe Gly Ile Phe Leu Ala Arg Thr Leu Ile Ser Asp Ile Glu
250 255 260

gca gtg aag acc ggc cat cac ttc tgaggagcag agttgaggga gccgagctga 935
Ala Val Lys Thr Gly His His Phe
265 270

gccacgctgg gaggccagag cctttctctg ccatcagccc tacgtccaga gggagaggag 995
ccgacacccc cagagccagt gcccacatctt aagcatcagc gtgacgtgac ctctctgttt 1055
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<211> 270
<212> PRT
<213> Homo sapiens

<400> 16
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Tyr Leu Leu Phe Ser Tyr Asn Ile Ile Phe Trp Leu Ala Gly Val Val
20 25 30
Phe Leu Gly Val Gly Leu Trp Ala Trp Ser Glu Lys Gly Val Leu Ser
35 40 45
Asp Leu Thr Lys Val Thr Arg Met His Gly Ile Asp Pro Ala Val Leu
50 55 60
Val Leu Met Val Gly Ala Val Met Phe Thr Leu Gly Phe Ala Gly Arg
65 70 75 80
Val Gly Ala Arg Arg Glu Asn Ile Cys Leu Leu Asn Phe Phe Cys Gly
85 90 95
Thr Ile Val Leu Ile Phe Phe Leu Glu Leu Ala Val Ala Val Leu Ala
100 105 110

Phe	Leu	Phe	Gln	Asp	Trp	Val	Arg	Asp	Arg	Phe	Arg	Glu	Phe	Phe	Glu
	115						120					125			
Ser	Asn	Ile	Lys	Ser	Tyr	Arg	Asp	Asp	Ile	Asp	Leu	Gln	Asn	Leu	Ile
	130					135					140				
Asp	Ser	Leu	Gln	Lys	Ala	Asn	Gln	Cys	Cys	Gly	Ala	Tyr	Gly	Pro	Glu
145					150					155					160
Asp	Trp	Asp	Leu	Asn	Val	Tyr	Phe	Asn	Cys	Ser	Gly	Ala	Ser	Tyr	Ser
				165					170					175	
Arg	Glu	Lys	Cys	Gly	Val	Pro	Phe	Ser	Cys	Cys	Val	Pro	Asp	Pro	Ala
			180					185					190		
Gln	Lys	Val	Val	Asn	Thr	Gln	Cys	Gly	Tyr	Asp	Val	Arg	Ile	Gln	Leu
	195						200					205			
Lys	Ser	Lys	Trp	Asp	Glu	Ser	Ile	Phe	Thr	Lys	Gly	Cys	Ile	Gln	Ala
	210					215					220				
Leu	Glu	Ser	Trp	Leu	Pro	Arg	Asn	Ile	Tyr	Ile	Val	Ala	Gly	Val	Phe
225					230					235					240
Ile	Ala	Ile	Ser	Leu	Leu	Gln	Ile	Phe	Gly	Ile	Phe	Leu	Ala	Arg	Thr
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Leu	Ile	Ser	Asp	Ile	Glu	Ala	Val	Lys	Thr	Gly	His	His	Phe		
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<220>
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 <222> (51)..(983)

<400> 17																	
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												1					
aac	ccc	agc	gcc	cca	cca	cca	tat	gaa	gac	cg	c	aac	ccc	ctg	tac	cca	104
Asn	Pro	Ser	Ala	Pro	Pro	Pro	Tyr	Glu	Asp	Arg	Asn	Pro	Pro	Leu	Tyr	Pro	
			5				10						15				
ggc	cct	ctg	ccc	cct	ggg	ggc	tat	ggg	cag	cca	tct	gtc	ctg	cca	gga		152
Gly	Pro	Leu	Pro	Pro	Gly	Gly	Tyr	Gly	Gln	Pro	Ser	Val	Leu	Pro	Gly		
	20					25					30						
ggg	tat	cct	gcc	tac	cct	ggc	tac	ccg	cag	cct	ggc	tac	ggt	cac	cct		200
Gly	Tyr	Pro	Ala	Tyr	Pro	Gly	Tyr	Pro	Gln	Pro	Gly	Tyr	Gly	His	Pro		
	35				40				45						50		

gct ggc tac cca cag ccc atg ccc ccc acc cac ccg atg ccc atg aac	248
Ala Gly Tyr Pro Gln Pro Met Pro Pro Thr His Pro Met Pro Met Asn	
55 60 65	
tac ggc cca ggc cat ggc tat gat ggg gag gag aga gcg gtg agt gat	296
Tyr Gly Pro Gly His Gly Tyr Asp Gly Glu Glu Arg Ala Val Ser Asp	
70 75 80	
agc ttc ggg cct gga gaa tgg gat gac cgg aaa gtg cga cac act ttt	344
Ser Phe Gly Pro Gly Glu Trp Asp Asp Arg Lys Val Arg His Thr Phe	
85 90 95	
atc cga aag gtt tac tcc atc atc tcc ggg cag ctg ctc atc act ggg	392
Ile Arg Lys Val Tyr Ser Ile Ile Ser Gly Gln Leu Leu Ile Thr Gly	
100 105 110	
gcc atc att gct atc ttc acc ttt ggg gaa cct gtc agc gcc ttt ggc	440
Ala Ile Ile Ala Ile Phe Thr Phe Gly Glu Pro Val Ser Ala Phe Gly	
115 120 125 130	
agg aga aat gtg gct gtc tac tac gtg tcc tat gct gtc ttc agt gtc	488
Arg Arg Asn Val Ala Val Tyr Tyr Val Ser Tyr Ala Val Phe Ser Val	
135 140 145	
acc tac ctg atc ctt gcc tgc tgc cag gga ccc aga cgc cgt ttc cca	536
Thr Tyr Leu Ile Leu Ala Cys Cys Gln Gly Pro Arg Arg Arg Phe Pro	
150 155 160	
tgg aac atc att ctg ctg acc ctt ttt act ttt gcc atg ggc ttc atg	584
Trp Asn Ile Ile Leu Leu Thr Leu Phe Thr Phe Ala Met Gly Phe Met	
165 170 175	
acg ggc acc att tcc agt atg tac caa acc aaa gcc gtc atc att gca	632
Thr Gly Thr Ile Ser Ser Met Tyr Gln Thr Lys Ala Val Ile Ile Ala	
180 185 190	
atg atc atc act gcg gtg gta tcc att tca gtc acc atc ttc tgc ttt	680
Met Ile Ile Thr Ala Val Val Ser Ile Ser Val Thr Ile Phe Cys Phe	
195 200 205 210	
cag acc aag gtg gac ttc acc tcg tgc aca ggc ctc ttc tgt gtc ctg	728
Gln Thr Lys Val Asp Phe Thr Ser Cys Thr Gly Leu Phe Cys Val Leu	
215 220 225	
gga att gtg ctc ctg gtg act ggg att gtc act agc att gtg ctc tac	776
Gly Ile Val Leu Leu Val Thr Gly Ile Val Thr Ser Ile Val Leu Tyr	
230 235 240	
ttc caa tac gtt tac tgg ctc cac atg ctc tat gct gct ctg ggg gcc	824
Phe Gln Tyr Val Tyr Trp Leu His Met Leu Tyr Ala Ala Leu Gly Ala	
245 250 255	
att tgt ttc acc ctg ttc ctg gct tac gac aca cag ctg gtc ctg ggg	872
Ile Cys Phe Thr Leu Phe Leu Ala Tyr Asp Thr Gln Leu Val Leu Gly	
260 265 270	

aac cgg aag cac acc atc agc ccc gag gac tac atc act ggc gcc ctg 920
 Asn Arg Lys His Thr Ile Ser Pro Glu Asp Tyr Ile Thr Gly Ala Leu
 275 280 285 290

cag att tac aca gac atc atc tac atc ttc acc ttt gtg ctg cag ctg 968
 Gln Ile Tyr Thr Asp Ile Ile Tyr Ile Phe Thr Phe Val Leu Gln Leu
 295 300 305

atg ggg gat cgc aat taaggagcaa gccccattt tcacccgac ctgggctctc 1023
 Met Gly Asp Arg Asn
 310

ccttccaagc tagagggctg ggccctatga ctgtggctctg ggcttttaggc ccctttcctt 1083
 ccccttgagt aacatgccca gtttcctttc tgtcctggag acaggtggcc tctctggcta 1143
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 <212> PRT
 <213> Homo sapiens

<400> 18
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 35 40 45
 His Pro Ala Gly Tyr Pro Gln Pro Met Pro Pro Thr His Pro Met Pro
 50 55 60

Met Asn Tyr Gly Pro Gly His Gly Tyr Asp Gly Glu Glu Arg Ala Val
 65 70 75 80
 Ser Asp Ser Phe Gly Pro Gly Glu Trp Asp Asp Arg Lys Val Arg His
 85 90 95
 Thr Phe Ile Arg Lys Val Tyr Ser Ile Ile Ser Gly Gln Leu Leu Ile
 100 105 110
 Thr Gly Ala Ile Ile Ala Ile Phe Thr Phe Gly Glu Pro Val Ser Ala
 115 120 125
 Phe Gly Arg Arg Asn Val Ala Val Tyr Tyr Val Ser Tyr Ala Val Phe
 130 135 140
 Ser Val Thr Tyr Leu Ile Leu Ala Cys Cys Gln Gly Pro Arg Arg Arg
 145 150 155 160
 Phe Pro Trp Asn Ile Ile Leu Leu Thr Leu Phe Thr Phe Ala Met Gly
 165 170 175
 Phe Met Thr Gly Thr Ile Ser Ser Met Tyr Gln Thr Lys Ala Val Ile
 180 185 190
 Ile Ala Met Ile Ile Thr Ala Val Val Ser Ile Ser Val Thr Ile Phe
 195 200 205
 Cys Phe Gln Thr Lys Val Asp Phe Thr Ser Cys Thr Gly Leu Phe Cys
 210 215 220
 Val Leu Gly Ile Val Leu Leu Val Thr Gly Ile Val Thr Ser Ile Val
 225 230 235 240
 Leu Tyr Phe Gln Tyr Val Tyr Trp Leu His Met Leu Tyr Ala Ala Leu
 245 250 255
 Gly Ala Ile Cys Phe Thr Leu Phe Leu Ala Tyr Asp Thr Gln Leu Val
 260 265 270
 Leu Gly Asn Arg Lys His Thr Ile Ser Pro Glu Asp Tyr Ile Thr Gly
 275 280 285
 Ala Leu Gln Ile Tyr Thr Asp Ile Ile Tyr Ile Phe Thr Phe Val Leu
 290 295 300
 Gln Leu Met Gly Asp Arg Asn
 305 310

<210> 19
 <211> 1686
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (372)..(1277)

<220>

<221> misc feature

<222> (1490)..(1630)

<223> an n may be any one of a or t or g or c

<400> 19

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taagaaataa tatttgaaat taatataaaa tgaagctaca gaaggcataa gtaagtccaa 180
atgttggtc tttgaaagac tattaaataa ttacacagaa agtctaataa agagaaaaga 240
gagaaaaaaa ctgtcagaat gctaccgaac tgtactgctt ctacagtgaag aacacggatc 300
tgacttgtcg gcagcccaag tgtgacaagt gcaatgctgc ctatcctcac ctggctcacc 360
tgccatctgc c atg gca gac tca tcc ttc cgg ttt cct cgc aca tgg tgg 410
          Met Ala Asp Ser Ser Phe Arg Phe Pro Arg Thr Trp Trp
            1              5              10

cag tct gcg gag gat gtg cac aga gaa aag atc cag tta gac ctg gaa 458
Gln Ser Ala Glu Asp Val His Arg Glu Lys Ile Gln Leu Asp Leu Glu
      15              20              25

gct gaa ttc tac ttc act cac cta att gtg atg ttc aag tcc ccc agg 506
Ala Glu Phe Tyr Phe Thr His Leu Ile Val Met Phe Lys Ser Pro Arg
      30              35              40              45

ccg gct gcc atg gtg ctg gac cgc tcc cag gac ttt ggg aaa aca tgg 554
Pro Ala Ala Met Val Leu Asp Arg Ser Gln Asp Phe Gly Lys Thr Trp
            50              55              60

aag cct tat aag tac ttt gcg act aac tgc tcc gct aca ttt ggc ctg 602
Lys Pro Tyr Lys Tyr Phe Ala Thr Asn Cys Ser Ala Thr Phe Gly Leu
            65              70              75

gaa gat gat gtt gtc aag aag ggc gct att tgt act tct aaa tac tcc 650
Glu Asp Asp Val Val Lys Lys Gly Ala Ile Cys Thr Ser Lys Tyr Ser
            80              85              90

agt cct ttt cca tgc act gga gga gag gtt att ttc aaa gct ttg tca 698
Ser Pro Phe Pro Cys Thr Gly Gly Glu Val Ile Phe Lys Ala Leu Ser
            95              100              105

cca cca tac gat aca gag aac cct tac agt gcc aaa gtt cag gag cag 746
Pro Pro Tyr Asp Thr Glu Asn Pro Tyr Ser Ala Lys Val Gln Glu Gln
      110              115              120              125

ctg aag atc acc aac ctt cgc gtg cag ctg ctg aaa cga cag tct tgt 794
Leu Lys Ile Thr Asn Leu Arg Val Gln Leu Leu Lys Arg Gln Ser Cys
            130              135              140

ccc tgt cag aga aat gac ctg aac gaa gag cct caa cat ttt aca cac 842
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Pro Cys Gln Arg Asn Asp Leu Asn Glu Glu Pro Gln His Phe Thr His	
145	150 155
tat gca atc tat gat ttc att gtc aag ggc agc tgc ttc tgc aat ggc	890
Tyr Ala Ile Tyr Asp Phe Ile Val Lys Gly Ser Cys Phe Cys Asn Gly	
160	165 170
cac gct gat caa tgc ata cct gtt cat ggc ttc aga cct gtc aag gcc	938
His Ala Asp Gln Cys Ile Pro Val His Gly Phe Arg Pro Val Lys Ala	
175	180 185
cca gga aca ttc cac atg gtc cat ggg aag tgt atg tgt aag cac aac	986
Pro Gly Thr Phe His Met Val His Gly Lys Cys Met Cys Lys His Asn	
190	195 200 205
aca gca ggc agc cac tgc cag cac tgt gcc ccg tta tac aat gac cgg	1034
Thr Ala Gly Ser His Cys Gln His Cys Ala Pro Leu Tyr Asn Asp Arg	
210	215 220
cca tgg gag gca gct gat ggc aaa acg ggg gct ccc aac gag tgc aga	1082
Pro Trp Glu Ala Ala Asp Gly Lys Thr Gly Ala Pro Asn Glu Cys Arg	
225	230 235
acc tgc aag tgt aat ggg cat gct gat acc tgt cac ttc gac gtt aat	1130
Thr Cys Lys Cys Asn Gly His Ala Asp Thr Cys His Phe Asp Val Asn	
240	245 250
gtg tgg gag gca tca ggg aat cgt agt ggt ggt gtc tgt gat gac tgt	1178
Val Trp Glu Ala Ser Gly Asn Arg Ser Gly Gly Val Cys Asp Asp Cys	
255	260 265
cag cac aac aca gaa gga cag tat tgc cag agg tgc aag cca ggc ttc	1226
Gln His Asn Thr Glu Gly Gln Tyr Cys Gln Arg Cys Lys Pro Gly Phe	
270	275 280 285
tat cgt gac ctg cgg aga ccc ttc tca gct cca gat gct tgc aaa cgt	1274
Tyr Arg Asp Leu Arg Arg Pro Phe Ser Ala Pro Asp Ala Cys Lys Arg	
290	295 300
aag taacctgtgg tttccagaaa ataggctgat ttgtacaaga gatgaatctc	1327
Lys	
tttatccctc attctgctaa cccaagagaa ggaggtcatt gaggttctga gataacacac	1387
ttacagatat cggttaattt cttcattgat aagaagcaag aattttcaac cattgggtga	1447
aaacagtata atattcatca aaagtaattt cctttctcat tctncataaa gtaaaaatta	1507
ttccctatac gctgcatttt ggtaaacagg atgactaata gaaaaaaaaa tgatgaanaa	1567
ggagactatt taagaactta agactacttg ggagtagaag gtagacaata atggactcan	1627
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<210> 20

<211> 302

<212> PRT

<213> Homo sapiens

<400> 20

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Glu	Asp	Val	His	Arg	Glu	Lys	Ile	Gln	Leu	Asp	Leu	Glu	Ala	Glu	Phe		
			20					25					30				
Tyr	Phe	Thr	His	Leu	Ile	Val	Met	Phe	Lys	Ser	Pro	Arg	Pro	Ala	Ala		
		35					40					45					
Met	Val	Leu	Asp	Arg	Ser	Gln	Asp	Phe	Gly	Lys	Thr	Trp	Lys	Pro	Tyr		
	50					55					60						
Lys	Tyr	Phe	Ala	Thr	Asn	Cys	Ser	Ala	Thr	Phe	Gly	Leu	Glu	Asp	Asp		
65					70					75					80		
Val	Val	Lys	Lys	Gly	Ala	Ile	Cys	Thr	Ser	Lys	Tyr	Ser	Ser	Pro	Phe		
				85					90					95			
Pro	Cys	Thr	Gly	Gly	Glu	Val	Ile	Phe	Lys	Ala	Leu	Ser	Pro	Pro	Tyr		
			100					105					110				
Asp	Thr	Glu	Asn	Pro	Tyr	Ser	Ala	Lys	Val	Gln	Glu	Gln	Leu	Lys	Ile		
		115					120					125					
Thr	Asn	Leu	Arg	Val	Gln	Leu	Leu	Lys	Arg	Gln	Ser	Cys	Pro	Cys	Gln		
	130					135					140						
Arg	Asn	Asp	Leu	Asn	Glu	Glu	Pro	Gln	His	Phe	Thr	His	Tyr	Ala	Ile		
145					150					155					160		
Tyr	Asp	Phe	Ile	Val	Lys	Gly	Ser	Cys	Phe	Cys	Asn	Gly	His	Ala	Asp		
			165						170					175			
Gln	Cys	Ile	Pro	Val	His	Gly	Phe	Arg	Pro	Val	Lys	Ala	Pro	Gly	Thr		
		180						185					190				
Phe	His	Met	Val	His	Gly	Lys	Cys	Met	Cys	Lys	His	Asn	Thr	Ala	Gly		
		195					200					205					
Ser	His	Cys	Gln	His	Cys	Ala	Pro	Leu	Tyr	Asn	Asp	Arg	Pro	Trp	Glu		
	210					215					220						
Ala	Ala	Asp	Gly	Lys	Thr	Gly	Ala	Pro	Asn	Glu	Cys	Arg	Thr	Cys	Lys		
225					230					235					240		
Cys	Asn	Gly	His	Ala	Asp	Thr	Cys	His	Phe	Asp	Val	Asn	Val	Trp	Glu		
			245						250					255			
Ala	Ser	Gly	Asn	Arg	Ser	Gly	Gly	Val	Cys	Asp	Asp	Cys	Gln	His	Asn		
			260					265					270				
Thr	Glu	Gly	Gln	Tyr	Cys	Gln	Arg	Cys	Lys	Pro	Gly	Phe	Tyr	Arg	Asp		
		275					280					285					

Leu Arg Arg Pro Phe Ser Ala Pro Asp Ala Cys Lys Arg Lys
 290 295 300

<210> 21
 <211> 2010
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (243)..(1658)

<400> 21

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ggagccggac acttgtctcc cgtctccgag ctgctcccca cccctggagg agagaccccc 180
ccctcggctc ggcgccttct gcgtctcccg gctgggtggg aagcctctgc gccgccggca 240

cc atg agt gaa cag agt atc tgt cag gca aga gct gct gtg atg gtt      287
  Met Ser Glu Gln Ser Ile Cys Gln Ala Arg Ala Ala Val Met Val
    1             5             10             15

tat gat gat gcc aat aag aag tgg gtg cca gct ggt ggc tca act gga      335
Tyr Asp Asp Ala Asn Lys Lys Trp Val Pro Ala Gly Gly Ser Thr Gly
          20             25             30

ttc agc aga gtt cat atc tat cac cat aca ggc aac aac aca ttc aga      383
Phe Ser Arg Val His Ile Tyr His His Thr Gly Asn Asn Thr Phe Arg
          35             40             45

gtg gtg ggc agg aag att cag gac cat cag gtc gtg ata aac tgt gcc      431
Val Val Gly Arg Lys Ile Gln Asp His Gln Val Val Ile Asn Cys Ala
          50             55             60

att cct aaa ggg ttg aag tac aat caa gct aca cag acc ttc cac cag      479
Ile Pro Lys Gly Leu Lys Tyr Asn Gln Ala Thr Gln Thr Phe His Gln
          65             70             75

tgg cga gat gct aga cag gtg tat ggt ctc aac ttt ggc agc aaa gag      527
Trp Arg Asp Ala Arg Gln Val Tyr Gly Leu Asn Phe Gly Ser Lys Glu
          80             85             90

gat gcc aat gtc ttc gca agt gcc atg atg cat gcc tta gaa gtg tta      575
Asp Ala Asn Val Phe Ala Ser Ala Met Met His Ala Leu Glu Val Leu
          100            105            110

aat tca cag gaa aca ggg cca aca ttg cct aga caa aac tca caa cta      623
Asn Ser Gln Glu Thr Gly Pro Thr Leu Pro Arg Gln Asn Ser Gln Leu
          115            120            125

cct gct caa gtt caa aat ggc cca tcc caa gaa gaa ttg gaa att caa      671

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Pro	Ala	Gln	Val	Gln	Asn	Gly	Pro	Ser	Gln	Glu	Glu	Leu	Glu	Ile	Gln		
	130						135					140					
aga	aga	caa	cta	caa	gaa	cag	caa	cgg	caa	aag	gag	ctg	gag	cgg	gaa	719	
Arg	Arg	Gln	Leu	Gln	Glu	Gln	Gln	Arg	Gln	Lys	Glu	Leu	Glu	Arg	Glu		
	145					150					155						
agg	ctg	aag	cga	gaa	aga	atg	gaa	aga	gaa	agg	aag	aag	aga	gag	agg	767	
Arg	Leu	Lys	Arg	Glu	Arg	Met	Glu	Arg	Glu	Arg	Lys	Lys	Arg	Glu	Arg		
	160				165					170					175		
tta	gaa	agg	gaa	agg	ctg	gag	agg	gag	cga	ctg	gaa	caa	gaa	cag	ctg	815	
Leu	Glu	Arg	Glu	Arg	Leu	Glu	Arg	Glu	Arg	Leu	Glu	Gln	Glu	Gln	Leu		
				180					185					190			
gag	aga	gag	aga	caa	gaa	cgg	gaa	cgg	cag	gaa	cgc	ctg	gag	cgg	cag	863	
Glu	Arg	Glu	Arg	Gln	Glu	Arg	Glu	Arg	Gln	Glu	Arg	Leu	Glu	Arg	Gln		
			195					200					205				
gaa	cgc	ctg	gag	cgg	cag	gaa	cgc	ctg	gag	cgg	cag	gaa	cgc	ctg	gat	911	
Glu	Arg	Leu	Glu	Arg	Gln	Glu	Arg	Leu	Glu	Arg	Gln	Glu	Arg	Leu	Asp		
		210					215					220					
cgg	gag	agg	caa	gaa	aga	caa	gaa	cga	gag	agg	ctg	gag	aga	ctg	gaa	959	
Arg	Glu	Arg	Gln	Glu	Arg	Gln	Glu	Arg	Glu	Arg	Leu	Glu	Arg	Leu	Glu		
	225					230					235						
cgg	gag	agg	caa	gaa	agg	gag	cga	caa	gag	cag	tta	gaa	agg	gaa	cag	1007	
Arg	Glu	Arg	Gln	Glu	Arg	Glu	Arg	Gln	Glu	Gln	Leu	Glu	Arg	Glu	Gln		
	240				245					250					255		
ctg	gaa	tgg	gag	aga	gag	cgc	aga	ata	tca	agt	gct	gct	gcc	cct	gcc	1055	
Leu	Glu	Trp	Glu	Arg	Glu	Arg	Arg	Ile	Ser	Ser	Ala	Ala	Ala	Pro	Ala		
				260				265					270				
tct	gtt	gag	act	cct	cta	aac	tct	gtg	ctg	gga	gac	tct	tct	gct	tct	1103	
Ser	Val	Glu	Thr	Pro	Leu	Asn	Ser	Val	Leu	Gly	Asp	Ser	Ser	Ala	Ser		
			275					280					285				
gag	cca	ggc	ttg	cag	gca	gcc	tct	cag	ccg	gcc	gag	act	cca	tcc	caa	1151	
Glu	Pro	Gly	Leu	Gln	Ala	Ala	Ser	Gln	Pro	Ala	Glu	Thr	Pro	Ser	Gln		
		290					295					300					
cag	gaa	gac	aat	cgc	cct	tta	act	gga	ctt	gca	gct	gca	att	gcc	gga	1199	
Gln	Glu	Asp	Asn	Arg	Pro	Leu	Thr	Gly	Leu	Ala	Ala	Ala	Ile	Ala	Gly		
	305					310				315							
gca	aaa	ctt	agg	aaa	gtg	tca	cgg	atg	gag	gat	acc	tct	ttc	cca	agt	1247	
Ala	Lys	Leu	Arg	Lys	Val	Ser	Arg	Met	Glu	Asp	Thr	Ser	Phe	Pro	Ser		
	320				325					330					335		
gga	ggg	aat	gct	att	ggg	gtg	aac	tcc	gcc	tca	tct	aaa	aca	gat	aca	1295	
Gly	Gly	Asn	Ala	Ile	Gly	Val	Asn	Ser	Ala	Ser	Ser	Lys	Thr	Asp	Thr		
				340				345						350			
ggc	cgt	gga	aat	gga	ccc	ctt	cct	tta	ggg	ggg	agt	ggg	tta	atg	gaa	1343	
Gly	Arg	Gly	Asn	Gly	Pro	Leu	Pro	Leu	Gly	Gly	Ser	Gly	Leu	Met	Glu		

355	360	365	
gaa atg agt gcc ctg ctg gcc acg agg aga aga att gct gaa aag gga			1391
Glu Met Ser Ala Leu Leu Ala Thr Arg Arg Arg Ile Ala Glu Lys Gly			
370	375	380	
tca aca ata gaa aca gaa caa aaa gag gac aaa ggt gaa gat tca gag			1439
Ser Thr Ile Glu Thr Glu Gln Lys Glu Asp Lys Gly Glu Asp Ser Glu			
385	390	395	
cct gta act tct aag gcc tct tca aca agt aca cct gaa cca aca aga			1487
Pro Val Thr Ser Lys Ala Ser Ser Thr Ser Thr Pro Glu Pro Thr Arg			
400	405	410	415
aaa cct tgg gaa aga aca aat aca atg aat ggc agc aag tca cct gtt			1535
Lys Pro Trp Glu Arg Thr Asn Thr Met Asn Gly Ser Lys Ser Pro Val			
420	425	430	
atc tcc aga cct cca agg aaa aat cag att gtt ttt gac aac agg tcc			1583
Ile Ser Arg Pro Pro Arg Lys Asn Gln Ile Val Phe Asp Asn Arg Ser			
435	440	445	
tat gat tca tta cac aga cca aaa tcc aca ccc gtt atc aca gcc cag			1631
Tyr Asp Ser Leu His Arg Pro Lys Ser Thr Pro Val Ile Thr Ala Gln			
450	455	460	
tgc caa tgg agt cca gac gga agg act tgactatgac aggctgaagc			1678
Cys Gln Trp Ser Pro Asp Gly Arg Thr			
465	470		
aggacatttt agatgaaatg agaaaagaat taacaaagct aaaagaagag ctcattgatg			1738
caatcaggca ggaactgagc aagtcaaata ctgcatagag gaacagacta aggagagata			1798
ggactttaat ctggaggaaa aatatcctac aaacaacaac tgttcacaac agcaaacccc			1858
tacatttatg agctgtaaga agaaaatgga gacaaacaga aggagggaaa aaccaaccta			1918
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<210> 22

<211> 472

<212> PRT

<213> Homo sapiens

<400> 22

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Asp Asp Ala Asn Lys Lys Trp Val Pro Ala Gly Gly Ser Thr Gly Phe			
20	25	30	
Ser Arg Val His Ile Tyr His His Thr Gly Asn Asn Thr Phe Arg Val			
35	40	45	

Val 50	Gly	Arg	Lys	Ile	Gln	Asp	His	Gln	Val	Val	Ile	Asn	Cys	Ala	Ile
Pro 65	Lys	Gly	Leu	Lys	Tyr	Asn	Gln	Ala	Thr	Gln	Thr	Phe	His	Gln	Trp 80
Arg	Asp	Ala	Arg	Gln	Val	Tyr	Gly	Leu	Asn	Phe	Gly	Ser	Lys	Glu	Asp
Ala	Asn	Val	Phe	Ala	Ser	Ala	Met	Met	His	Ala	Leu	Glu	Val	Leu	Asn
Ser	Gln	Glu	Thr	Gly	Pro	Thr	Leu	Pro	Arg	Gln	Asn	Ser	Gln	Leu	Pro
Ala	Gln	Val	Gln	Asn	Gly	Pro	Ser	Gln	Glu	Glu	Leu	Glu	Ile	Gln	Arg
Arg	Gln	Leu	Gln	Glu	Gln	Gln	Arg	Gln	Lys	Glu	Leu	Glu	Arg	Glu	Arg
Leu	Lys	Arg	Glu	Arg	Met	Glu	Arg	Glu	Arg	Lys	Lys	Arg	Glu	Arg	Leu
Glu	Arg	Glu	Arg	Leu	Glu	Arg	Glu	Arg	Leu	Glu	Gln	Glu	Gln	Leu	Glu
Arg	Glu	Arg	Gln	Glu	Arg	Glu	Arg	Gln	Glu	Arg	Leu	Glu	Arg	Gln	Glu
Arg	Leu	Glu	Arg	Gln	Glu	Arg	Leu	Glu	Arg	Gln	Glu	Arg	Leu	Asp	Arg
Glu	Arg	Gln	Glu	Arg	Gln	Glu	Arg	Glu	Arg	Leu	Glu	Arg	Leu	Glu	Arg
Glu	Arg	Gln	Glu	Arg	Glu	Arg	Gln	Glu	Gln	Leu	Glu	Arg	Glu	Gln	Leu
Glu	Trp	Glu	Arg	Glu	Arg	Arg	Ile	Ser	Ser	Ala	Ala	Ala	Pro	Ala	Ser
Val	Glu	Thr	Pro	Leu	Asn	Ser	Val	Leu	Gly	Asp	Ser	Ser	Ala	Ser	Glu
Pro	Gly	Leu	Gln	Ala	Ala	Ser	Gln	Pro	Ala	Glu	Thr	Pro	Ser	Gln	Gln
Glu	Asp	Asn	Arg	Pro	Leu	Thr	Gly	Leu	Ala	Ala	Ala	Ile	Ala	Gly	Ala
Lys	Leu	Arg	Lys	Val	Ser	Arg	Met	Glu	Asp	Thr	Ser	Phe	Pro	Ser	Gly
Gly	Asn	Ala	Ile	Gly	Val	Asn	Ser	Ala	Ser	Ser	Lys	Thr	Asp	Thr	Gly

Arg Gly Asn Gly Pro Leu Pro Leu Gly Gly Ser Gly Leu Met Glu Glu
 355 360 365
 Met Ser Ala Leu Leu Ala Thr Arg Arg Arg Ile Ala Glu Lys Gly Ser
 370 375 380
 Thr Ile Glu Thr Glu Gln Lys Glu Asp Lys Gly Glu Asp Ser Glu Pro
 385 390 395 400
 Val Thr Ser Lys Ala Ser Ser Thr Ser Thr Pro Glu Pro Thr Arg Lys
 405 410 415
 Pro Trp Glu Arg Thr Asn Thr Met Asn Gly Ser Lys Ser Pro Val Ile
 420 425 430
 Ser Arg Pro Pro Arg Lys Asn Gln Ile Val Phe Asp Asn Arg Ser Tyr
 435 440 445
 Asp Ser Leu His Arg Pro Lys Ser Thr Pro Val Ile Thr Ala Gln Cys
 450 455 460
 Gln Trp Ser Pro Asp Gly Arg Thr
 465 470

<210> 23
 <211> 1952
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (243)..(1715)

<400> 23
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 ctcccggccg gcgcctcggc tttgtgcgag gagatggtgt agccccctgg ccgccgaaga 120
 ggagccggac acttgtctcc cgtctccgag ctgctcccca cccctggagg agagaccccc 180
 ccctcggtc gggccttct gcgtctcccg gctggtgggg aagcctctgc gccgccggca 240
 cc atg agt gaa cag agt atc tgt cag gca aga gct gct gtg atg gtt 287
 Met Ser Glu Gln Ser Ile Cys Gln Ala Arg Ala Ala Val Met Val
 1 5 10 15
 tat gat gat gcc aat aag aag tgg gtg cca gct ggt ggc tca act gga 335
 Tyr Asp Asp Ala Asn Lys Lys Trp Val Pro Ala Gly Gly Ser Thr Gly
 20 25 30
 ttc agc aga gtt cat atc tat cac cat aca ggc aac aac aca ttc aga 383
 Phe Ser Arg Val His Ile Tyr His His Thr Gly Asn Asn Thr Phe Arg
 35 40 45

gtg gtg ggc agg aag att cag gac cat cag gtc gtg ata aac tgt gcc	431
Val Val Gly Arg Lys Ile Gln Asp His Gln Val Val Ile Asn Cys Ala	
50 55 60	
att cct aaa ggg ttg aag tac aat caa gct aca cag acc ttc cac cag	479
Ile Pro Lys Gly Leu Lys Tyr Asn Gln Ala Thr Gln Thr Phe His Gln	
65 70 75	
tgg cga gat gct aga cag gtg tat ggt ctc aac ttt ggc agc aaa gag	527
Trp Arg Asp Ala Arg Gln Val Tyr Gly Leu Asn Phe Gly Ser Lys Glu	
80 85 90 95	
gat gcc aat gtc ttc gca agt gcc atg atg cat gcc tta gaa gtg tta	575
Asp Ala Asn Val Phe Ala Ser Ala Met Met His Ala Leu Glu Val Leu	
100 105 110	
aat tca cag gaa aca ggg cca aca ttg cct aga caa aac tca caa cta	623
Asn Ser Gln Glu Thr Gly Pro Thr Leu Pro Arg Gln Asn Ser Gln Leu	
115 120 125	
cct gct caa gtt caa aat ggc cca tcc caa gaa gaa ttg gaa att caa	671
Pro Ala Gln Val Gln Asn Gly Pro Ser Gln Glu Glu Leu Glu Ile Gln	
130 135 140	
aga aga caa cta caa gaa cag caa cgg caa aag gag ctg gag cgg gaa	719
Arg Arg Gln Leu Gln Glu Gln Gln Arg Gln Lys Glu Leu Glu Arg Glu	
145 150 155	
agg ctg aag cga gaa aga atg gaa aga gaa agg aag aag aga gag agg	767
Arg Leu Lys Arg Glu Arg Met Glu Arg Glu Arg Lys Lys Arg Glu Arg	
160 165 170 175	
tta gaa agg gaa agg ctg gag agg gag cga ctg gaa caa gaa cag ctg	815
Leu Glu Arg Glu Arg Leu Glu Arg Glu Arg Leu Glu Gln Glu Gln Leu	
180 185 190	
gag aga gag aga caa gaa cgg gaa cgg cag gaa cgc ctg gag cgg cag	863
Glu Arg Glu Arg Gln Glu Arg Glu Arg Gln Glu Arg Leu Glu Arg Gln	
195 200 205	
gaa cgc ctg gag cgg cag gaa cgc ctg gag cgg cag gaa cgc ctg gat	911
Glu Arg Leu Glu Arg Gln Glu Arg Leu Glu Arg Gln Glu Arg Leu Asp	
210 215 220	
cgg gag agg caa gaa aga caa gaa cga gag agg ctg gag aga ctg gaa	959
Arg Glu Arg Gln Glu Arg Gln Glu Arg Glu Arg Leu Glu Arg Leu Glu	
225 230 235	
cgg gag agg caa gaa agg gag cga caa gag cag tta gaa agg gaa cag	1007
Arg Glu Arg Gln Glu Arg Glu Arg Gln Glu Gln Leu Glu Arg Glu Gln	
240 245 250 255	
ctg gaa tgg gag aga gag cgc aga ata tca agt gct gct gcc cct gcc	1055
Leu Glu Trp Glu Arg Glu Arg Arg Ile Ser Ser Ala Ala Pro Ala	
260 265 270	
tct gtt gag act cct cta aac tct gtg ctg gga gac tct tct gct tct	1103

Ser Val Glu Thr Pro Leu Asn Ser Val Leu Gly Asp Ser Ser Ala Ser	
275	280
285	
gag cca ggc ttg cag gca gcc tct cag ccg gcc gag act cca tcc caa	1151
Glu Pro Gly Leu Gln Ala Ala Ser Gln Pro Ala Glu Thr Pro Ser Gln	
290	295
300	
cag gaa gac aat cgc cct tta act gga ctt gca gct gca att gcc gga	1199
Gln Glu Asp Asn Arg Pro Leu Thr Gly Leu Ala Ala Ala Ile Ala Gly	
305	310
315	
gca aaa ctt agg aaa gtg tca cgg atg gag gat acc tct ttc cca agt	1247
Ala Lys Leu Arg Lys Val Ser Arg Met Glu Asp Thr Ser Phe Pro Ser	
320	325
330	335
gga ggg aat gct att ggt gtg aac tcc gcc tca tct aaa aca gat aca	1295
Gly Gly Asn Ala Ile Gly Val Asn Ser Ala Ser Ser Lys Thr Asp Thr	
340	345
350	
ggc cgt gga aat gga ccc ctt cct tta ggg ggt agt ggt tta atg gaa	1343
Gly Arg Gly Asn Gly Pro Leu Pro Leu Gly Gly Ser Gly Leu Met Glu	
355	360
365	
gaa atg agt gcc ctg ctg gcc acg agg aga aga att gct gaa aag gga	1391
Glu Met Ser Ala Leu Leu Ala Thr Arg Arg Arg Ile Ala Glu Lys Gly	
370	375
380	
tca aca ata gaa aca gaa caa aaa gag gac aaa ggt gaa gat tca gag	1439
Ser Thr Ile Glu Thr Glu Gln Lys Glu Asp Lys Gly Glu Asp Ser Glu	
385	390
395	
cct gta act tct aag gcc tct tca aca agt aca cct gaa cca aca aga	1487
Pro Val Thr Ser Lys Ala Ser Ser Thr Ser Thr Pro Glu Pro Thr Arg	
400	405
410	415
aaa cct tgg gaa aga aca aat aca atg aat ggc agc aag tca cct gtt	1535
Lys Pro Trp Glu Arg Thr Asn Thr Met Asn Gly Ser Lys Ser Pro Val	
420	425
430	
atc tcc aga cca aaa tcc aca ccc tta tca cag ccc agt gcc aat gga	1583
Ile Ser Arg Pro Lys Ser Thr Pro Leu Ser Gln Pro Ser Ala Asn Gly	
435	440
445	
gtc cag acg gaa gga ctt gac tat gac agg ctg aag cag gac att tta	1631
Val Gln Thr Glu Gly Leu Asp Tyr Asp Arg Leu Lys Gln Asp Ile Leu	
450	455
460	
gat gaa atg aga aaa gaa tta aca aag cta aaa gaa gag ctc att gat	1679
Asp Glu Met Arg Lys Glu Leu Thr Lys Leu Lys Glu Glu Leu Ile Asp	
465	470
475	
gca atc agg cag gaa ctg agc aag tca aat act gca tagaggaaca	1725
Ala Ile Arg Gln Glu Leu Ser Lys Ser Asn Thr Ala	
480	485
490	
gactaaggag agataggact ttaatctgga ggaaaaatat cctacaaaca acaactgttc	1785

acaacagcaa acccctacat ttatgagctg taagaagaaa atggagacaa acagaaggag 1845
 ggaaaaacca acctactctg aaagccttca gacattatga ctctggtgat aagctctttc 1905
 cctctccggtt tgctgctttt ttctggccaa catcagaatg gtaacac 1952

<210> 24
 <211> 491
 <212> PRT
 <213> Homo sapiens

<400> 24
 Met Ser Glu Gln Ser Ile Cys Gln Ala Arg Ala Ala Val Met Val Tyr
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 Asp Asp Ala Asn Lys Lys Trp Val Pro Ala Gly Gly Ser Thr Gly Phe
 20 25 30
 Ser Arg Val His Ile Tyr His His Thr Gly Asn Asn Thr Phe Arg Val
 35 40 45
 Val Gly Arg Lys Ile Gln Asp His Gln Val Val Ile Asn Cys Ala Ile
 50 55 60
 Pro Lys Gly Leu Lys Tyr Asn Gln Ala Thr Gln Thr Phe His Gln Trp
 65 70 75 80
 Arg Asp Ala Arg Gln Val Tyr Gly Leu Asn Phe Gly Ser Lys Glu Asp
 85 90 95
 Ala Asn Val Phe Ala Ser Ala Met Met His Ala Leu Glu Val Leu Asn
 100 105 110
 Ser Gln Glu Thr Gly Pro Thr Leu Pro Arg Gln Asn Ser Gln Leu Pro
 115 120 125
 Ala Gln Val Gln Asn Gly Pro Ser Gln Glu Glu Leu Glu Ile Gln Arg
 130 135 140
 Arg Gln Leu Gln Glu Gln Gln Arg Gln Lys Glu Leu Glu Arg Glu Arg
 145 150 155 160
 Leu Lys Arg Glu Arg Met Glu Arg Glu Arg Lys Lys Arg Glu Arg Leu
 165 170 175
 Glu Arg Glu Arg Leu Glu Arg Glu Arg Leu Glu Gln Glu Gln Leu Glu
 180 185 190
 Arg Glu Arg Gln Glu Arg Glu Arg Gln Glu Arg Leu Glu Arg Gln Glu
 195 200 205
 Arg Leu Glu Arg Gln Glu Arg Leu Glu Arg Gln Glu Arg Leu Asp Arg
 210 215 220
 Glu Arg Gln Glu Arg Gln Glu Arg Glu Arg Leu Glu Arg Leu Glu Arg
 225 230 235 240

Glu	Arg	Gln	Glu	Arg	Glu	Arg	Gln	Glu	Gln	Leu	Glu	Arg	Glu	Gln	Leu			
				245					250					255				
Glu	Trp	Glu	Arg	Glu	Arg	Arg	Ile	Ser	Ser	Ala	Ala	Ala	Pro	Ala	Ser			
			260					265					270					
Val	Glu	Thr	Pro	Leu	Asn	Ser	Val	Leu	Gly	Asp	Ser	Ser	Ala	Ser	Glu			
		275					280					285						
Pro	Gly	Leu	Gln	Ala	Ala	Ser	Gln	Pro	Ala	Glu	Thr	Pro	Ser	Gln	Gln			
	290					295					300							
Glu	Asp	Asn	Arg	Pro	Leu	Thr	Gly	Leu	Ala	Ala	Ala	Ile	Ala	Gly	Ala			
305					310				315					320				
Lys	Leu	Arg	Lys	Val	Ser	Arg	Met	Glu	Asp	Thr	Ser	Phe	Pro	Ser	Gly			
			325						330					335				
Gly	Asn	Ala	Ile	Gly	Val	Asn	Ser	Ala	Ser	Ser	Lys	Thr	Asp	Thr	Gly			
		340						345					350					
Arg	Gly	Asn	Gly	Pro	Leu	Pro	Leu	Gly	Gly	Ser	Gly	Leu	Met	Glu	Glu			
		355					360					365						
Met	Ser	Ala	Leu	Leu	Ala	Thr	Arg	Arg	Arg	Ile	Ala	Glu	Lys	Gly	Ser			
	370					375					380							
Thr	Ile	Glu	Thr	Glu	Gln	Lys	Glu	Asp	Lys	Gly	Glu	Asp	Ser	Glu	Pro			
385					390					395					400			
Val	Thr	Ser	Lys	Ala	Ser	Ser	Thr	Ser	Thr	Pro	Glu	Pro	Thr	Arg	Lys			
			405						410					415				
Pro	Trp	Glu	Arg	Thr	Asn	Thr	Met	Asn	Gly	Ser	Lys	Ser	Pro	Val	Ile			
		420					425						430					
Ser	Arg	Pro	Lys	Ser	Thr	Pro	Leu	Ser	Gln	Pro	Ser	Ala	Asn	Gly	Val			
		435					440					445						
Gln	Thr	Glu	Gly	Leu	Asp	Tyr	Asp	Arg	Leu	Lys	Gln	Asp	Ile	Leu	Asp			
	450					455					460							
Glu	Met	Arg	Lys	Glu	Leu	Thr	Lys	Leu	Lys	Glu	Glu	Leu	Ile	Asp	Ala			
465					470					475					480			
Ile	Arg	Gln	Glu	Leu	Ser	Lys	Ser	Asn	Thr	Ala								
			485					490										

<210> 25

<211> 827

<212> DNA

<213> Homo sapiens

<220>

<221> CDS
<222> (233)..(601)

<400> 25

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gaatcacccg ctgatggttt ttgccagggc ctgaaacaac cagagagcta cgggaaagga 120
agggcttggc ttgccagagg aattttccaa gtgctcaaac gccaggctta cggcgctgt 180
gatccgtcca ggaggacaaa gtgggatttg aggatccact ccacttctgc tc atg gcg 238
Met Ala
1

cgc cag ggc ctg ccc ctg cac gtg gcc aca ctg ctg act ggg ctg ctg 286
Arg Gln Gly Leu Pro Leu His Val Ala Thr Leu Leu Thr Gly Leu Leu
5 10 15

gaa tgc ctg ggc ttt gct ggc gtc ctc ttt ggc tgg cct tca cta gtg 334
Glu Cys Leu Gly Phe Ala Gly Val Leu Phe Gly Trp Pro Ser Leu Val
20 25 30

ttt gtc ttc aag aat gaa gat tac ttt aag gat ctg tgt gga cca gat 382
Phe Val Phe Lys Asn Glu Asp Tyr Phe Lys Asp Leu Cys Gly Pro Asp
35 40 45 50

gct ggg ccg att ggc aat gcc aca ggg cag gct gac tgc aaa gcc cag 430
Ala Gly Pro Ile Gly Asn Ala Thr Gly Gln Ala Asp Cys Lys Ala Gln
55 60 65

gat gag agg ttc tca ctc atc ttc acc ctg ggg tcc ttc atg aac aac 478
Asp Glu Arg Phe Ser Leu Ile Phe Thr Leu Gly Ser Phe Met Asn Asn
70 75 80

ttc atg aca ttc ccc act ggc tac atc ttt gac cgg ttc aag acc acc 526
Phe Met Thr Phe Pro Thr Gly Tyr Ile Phe Asp Arg Phe Lys Thr Thr
85 90 95

gtg gca cgc ctc ata gcc ata ttt ttc tac acc acc gcc aca ctc atc 574
Val Ala Arg Leu Ile Ala Ile Phe Phe Tyr Thr Thr Ala Thr Leu Ile
100 105 110

ata gcc ttc acc tct gca gct tct tta tgaaaaaggc atcagcctca 621
Ile Ala Phe Thr Ser Ala Ala Ser Leu
115 120

gggcctcctt catcttcac tctgtctgca agtacctggc atgtagcacg cactttcctc 681
ctgatgcccc gggggcacat ccataccca ctgccccca actacagcta tggcctgtgc 741
cctgggaatg gcaccacaaa ggaagagaag gaaacagctg agcatgaaaa caggagagcta 801
cagtcaaagg agttcctttc agcgaa 827

<210> 26
<211> 123

<212> PRT
<213> Homo sapiens

<400> 26

Met	Ala	Arg	Gln	Gly	Leu	Pro	Leu	His	Val	Ala	Thr	Leu	Leu	Thr	Gly	
1				5					10					15		
Leu	Leu	Glu	Cys	Leu	Gly	Phe	Ala	Gly	Val	Leu	Phe	Gly	Trp	Pro	Ser	
		20						25					30			
Leu	Val	Phe	Val	Phe	Lys	Asn	Glu	Asp	Tyr	Phe	Lys	Asp	Leu	Cys	Gly	
		35					40					45				
Pro	Asp	Ala	Gly	Pro	Ile	Gly	Asn	Ala	Thr	Gly	Gln	Ala	Asp	Cys	Lys	
	50					55					60					
Ala	Gln	Asp	Glu	Arg	Phe	Ser	Leu	Ile	Phe	Thr	Leu	Gly	Ser	Phe	Met	
65					70					75					80	
Asn	Asn	Phe	Met	Thr	Phe	Pro	Thr	Gly	Tyr	Ile	Phe	Asp	Arg	Phe	Lys	
			85						90						95	
Thr	Thr	Val	Ala	Arg	Leu	Ile	Ala	Ile	Phe	Phe	Tyr	Thr	Thr	Ala	Thr	
		100						105						110		
Leu	Ile	Ile	Ala	Phe	Thr	Ser	Ala	Ala	Ser	Leu						
	115							120								

<210> 27
<211> 1063
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (48)..(944)

<400> 27

cttttttcag	ataacatctt	ctgagtcata	accagcctgg	gtccccc	atg	atc	gtg	56								
					Met	Ile	Val									
					1											
ggg	tcc	cct	cgg	gcc	ctg	aca	cag	ccc	ctg	ggt	ctc	ctt	cgc	ctg	ctg	104
Gly	Ser	Pro	Arg	Ala	Leu	Thr	Gln	Pro	Leu	Gly	Leu	Leu	Arg	Leu	Leu	
	5					10					15					
cag	ctg	gtg	tct	acc	tgc	gtg	gcc	ttc	tgc	ctg	gtg	gct	agc	gtg	ggc	152
Gln	Leu	Val	Ser	Thr	Cys	Val	Ala	Phe	Ser	Leu	Val	Ala	Ser	Val	Gly	
	20				25					30					35	
gcc	tgg	acg	ggg	tcc	atg	ggc	aac	tgg	tcc	atg	ttc	acc	tgg	tgc	ttc	200
Ala	Trp	Thr	Gly	Ser	Met	Gly	Asn	Trp	Ser	Met	Phe	Thr	Trp	Cys	Phe	
			40					45						50		
tgc	ttc	tcc	gtg	acc	ctg	atc	atc	ctc	atc	gtg	gag	ctg	tgc	ggg	ctc	248

Cys Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu	
55 60 65	
cag gcc cgc ttc ccc ctg tct tgg cgc aac ttc ccc atc acc ttc gcc	296
Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe Ala	
70 75 80	
tgc tat gcg gcc ctc ttc tgc ctc tcg gcc tcc atc atc tac ccc acc	344
Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr Pro Thr	
85 90 95	
acc tat gtc cag ttc ctg tcc cac gcc cgt tcg cgg gac cac gcc atc	392
Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp His Ala Ile	
100 105 110 115	
gcc gcc acc ttc ttc tcc tgc atc gcg tgt gtg gct tac gcc acc gaa	440
Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala Tyr Ala Thr Glu	
120 125 130	
gtg gcc tgg acc cgg gcc cgg ccc gcc gag atc act gcc tat atg gcc	488
Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile Thr Gly Tyr Met Ala	
135 140 145	
acc gta ccc ggg ctg ctg aag gtg ctg gag acc ttc gtt gcc tgc atc	536
Thr Val Pro Gly Leu Leu Lys Val Leu Glu Thr Phe Val Ala Cys Ile	
150 155 160	
atc ttc gcg ttc atc agc gac ccc aac ctg tac cag cac cag ccg gcc	584
Ile Phe Ala Phe Ile Ser Asp Pro Asn Leu Tyr Gln His Gln Pro Ala	
165 170 175	
ctg gag tgg tgc gtg gcg gtg tac gcc atc tgc ttc atc cta gcg gcc	632
Leu Glu Trp Cys Val Ala Val Tyr Ala Ile Cys Phe Ile Leu Ala Ala	
180 185 190 195	
atc gcc atc ctg ctg aac ctg ggg gag tgc acc aac gtg cta ccc atc	680
Ile Ala Ile Leu Leu Asn Leu Gly Glu Cys Thr Asn Val Leu Pro Ile	
200 205 210	
ccc ttc ccc agc ttc ctg tcg ggg ctg gcc ttg ctg tct gtc ctc ctc	728
Pro Phe Pro Ser Phe Leu Ser Gly Leu Ala Leu Leu Ser Val Leu Leu	
215 220 225	
tat gcc acc gcc ctt gtt ctc tgg ccc ctc tac cag ttc gat gag aag	776
Tyr Ala Thr Ala Leu Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys	
230 235 240	
tat ggc ggc cag cct cgg cgc tcg aga gat gta agc tgc agc cgc agc	824
Tyr Gly Gly Gln Pro Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser	
245 250 255	
cat gcc tac tac gtg tgt gcc tgg gac cgc cga ctg gct gtg gcc atc	872
His Ala Tyr Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile	
260 265 270 275	
ctg acg gcc atc aac cta ctg gcg tat gtg gct gac ctg gtg cac tct	920
Leu Thr Ala Ile Asn Leu Leu Ala Tyr Val Ala Asp Leu Val His Ser	

280

285

290

gcc cac ctg gtt ttt gtc aag gtc taagactctc ccaagaggct cccgttcct 974
 Ala His Leu Val Phe Val Lys Val
 295

ctccaacctc tttgttcttc ttgcccgagt tttctttatg gagtacttct ttcctccgcc 1034
 tttcctctgt tttcctcttc ctgtctccc 1063

<210> 28

<211> 299

<212> PRT

<213> Homo sapiens

<400> 28

Met Ile Val Gly Ser Pro Arg Ala Leu Thr Gln Pro Leu Gly Leu Leu
 1 5 10 15

Arg Leu Leu Gln Leu Val Ser Thr Cys Val Ala Phe Ser Leu Val Ala
 20 25 30

Ser Val Gly Ala Trp Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr
 35 40 45

Trp Cys Phe Cys Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu
 50 55 60

Cys Gly Leu Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile
 65 70 75 80

Thr Phe Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile
 85 90 95

Tyr Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp
 100 105 110

His Ala Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala Tyr
 115 120 125

Ala Thr Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile Thr Gly
 130 135 140

Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu Thr Phe Val
 145 150 155 160

Ala Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn Leu Tyr Gln His
 165 170 175

Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr Ala Ile Cys Phe Ile
 180 185 190

Leu Ala Ala Ile Ala Ile Leu Leu Asn Leu Gly Glu Cys Thr Asn Val
 195 200 205

Leu Pro Ile Pro Phe Pro Ser Phe Leu Ser Gly Leu Ala Leu Leu Ser

210	215	220
Val Leu Leu Tyr Ala Thr Ala Leu Val Leu Trp Pro Leu Tyr Gln Phe		
225	230	235 240
Asp Glu Lys Tyr Gly Gly Gln Pro Arg Arg Ser Arg Asp Val Ser Cys		
	245	250 255
Ser Arg Ser His Ala Tyr Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala		
	260	265 270
Val Ala Ile Leu Thr Ala Ile Asn Leu Leu Ala Tyr Val Ala Asp Leu		
	275	280 285
Val His Ser Ala His Leu Val Phe Val Lys Val		
290	295	

<210> 29
 <211> 1890
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1890)

<400> 29
 gga tcc ggt ttc cca gaa gat tct gag cca atc agt att tcg cat ggc 48
 Gly Ser Gly Phe Pro Glu Asp Ser Glu Pro Ile Ser Ile Ser His Gly
 1 5 10 15
 aac tat aca aaa cag tat ccg gtg ttt gtg ggc cac aag cca gga cgg 96
 Asn Tyr Thr Lys Gln Tyr Pro Val Phe Val Gly His Lys Pro Gly Arg
 20 25 30
 aac acc aca cag agg cac agg ctg gac atc cag atg att atg atc atg 144
 Asn Thr Thr Gln Arg His Arg Leu Asp Ile Gln Met Ile Met Ile Met
 35 40 45
 aac gga acc ctc tac att gct gct agg gac cat att tat act gtt gat 192
 Asn Gly Thr Leu Tyr Ile Ala Ala Arg Asp His Ile Tyr Thr Val Asp
 50 55 60
 ata gac aca tca cac acg gaa gaa att tat tgt agc aaa aaa ctg aca 240
 Ile Asp Thr Ser His Thr Glu Glu Ile Tyr Cys Ser Lys Lys Leu Thr
 65 70 75 80
 tgg aaa tct aga cag gcc gat gta gac aca tgc aga atg aag gga aaa 288
 Trp Lys Ser Arg Gln Ala Asp Val Asp Thr Cys Arg Met Lys Gly Lys
 85 90 95
 cat aag gat gag tgc cac aac ttt att aaa gtt ctt cta aag aaa aac 336
 His Lys Asp Glu Cys His Asn Phe Ile Lys Val Leu Leu Lys Lys Asn
 100 105 110

gat gat gca ttg ttt gtc tgt gga act aat gcc ttc aac cct tcc tgc	384
Asp Asp Ala Leu Phe Val Cys Gly Thr Asn Ala Phe Asn Pro Ser Cys	
115 120 125	
aga aac tat aag atg gat aca ttg gaa cca ttc ggg gat gaa ttc agc	432
Arg Asn Tyr Lys Met Asp Thr Leu Glu Pro Phe Gly Asp Glu Phe Ser	
130 135 140	
gga atg gcc aga tgc cca tat gat gcc aaa cat gcc aac gtt gca ctg	480
Gly Met Ala Arg Cys Pro Tyr Asp Ala Lys His Ala Asn Val Ala Leu	
145 150 155 160	
ttt gca gat gga aaa cta tac tca gcc aca gtg act gac ttc ctt gcc	528
Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr Val Thr Asp Phe Leu Ala	
165 170 175	
att gac gca gtc att tac cgg agt ctt gga gaa agc cct acc ctg cgg	576
Ile Asp Ala Val Ile Tyr Arg Ser Leu Gly Glu Ser Pro Thr Leu Arg	
180 185 190	
acc gtc aag cac gat tca aaa tgg ttg aaa gaa cca tac ttt gtt caa	624
Thr Val Lys His Asp Ser Lys Trp Leu Lys Glu Pro Tyr Phe Val Gln	
195 200 205	
gcc gtg gat tac gga gat tat atc tac ttc ttc ttc agg gaa ata gca	672
Ala Val Asp Tyr Gly Asp Tyr Ile Tyr Phe Phe Phe Arg Glu Ile Ala	
210 215 220	
gtg gag tat aac acc atg gga aag gta gtt ttc cca aga gtg gct cag	720
Val Glu Tyr Asn Thr Met Gly Lys Val Val Phe Pro Arg Val Ala Gln	
225 230 235 240	
gtt tgt aag aat gat atg gga gga tct caa aga gtc ctg gag aaa cag	768
Val Cys Lys Asn Asp Met Gly Gly Ser Gln Arg Val Leu Glu Lys Gln	
245 250 255	
tgg acg tcg ttc ctg aag gcg cgc ttg aac tgc tca gtt cct gga gac	816
Trp Thr Ser Phe Leu Lys Ala Arg Leu Asn Cys Ser Val Pro Gly Asp	
260 265 270	
tct cat ttt tat ttc aac att ctc cag gca gtt aca gat gtg att cgt	864
Ser His Phe Tyr Phe Asn Ile Leu Gln Ala Val Thr Asp Val Ile Arg	
275 280 285	
atc aac ggg cgt gat gtt gtc ctg gca acg ttt tct aca cct tat aac	912
Ile Asn Gly Arg Asp Val Val Leu Ala Thr Phe Ser Thr Pro Tyr Asn	
290 295 300	
agc atc cct ggg tct gca gtc tgt gcc tat gac atg ctt gac att gcc	960
Ser Ile Pro Gly Ser Ala Val Cys Ala Tyr Asp Met Leu Asp Ile Ala	
305 310 315 320	
agt gtt ttt act ggg aga ttc aag gaa cag aag tct cct gat tcc acc	1008
Ser Val Phe Thr Gly Arg Phe Lys Glu Gln Lys Ser Pro Asp Ser Thr	
325 330 335	
tgg aca cca gtt cct gat gaa cga gtt cct aag ccc agg cca ggt tgc	1056

Trp Thr Pro Val Pro Asp Glu Arg Val Pro Lys Pro Arg Pro Gly Cys	
340 345 350	
tgt gct ggc tca tcc tcc tta gaa aga tat gca acc tcc aat gag ttc	1104
Cys Ala Gly Ser Ser Ser Leu Glu Arg Tyr Ala Thr Ser Asn Glu Phe	
355 360 365	
cct gat gat acc ctg aac ttc atc aag acg cac ccg ctc atg gat gag	1152
Pro Asp Asp Thr Leu Asn Phe Ile Lys Thr His Pro Leu Met Asp Glu	
370 375 380	
gca gtg ccc tcc atc ttc aac agg cca tgg ttc ctg aga aca atg gtc	1200
Ala Val Pro Ser Ile Phe Asn Arg Pro Trp Phe Leu Arg Thr Met Val	
385 390 395 400	
aga tac cgc ctt acc aaa att gca gtg gac aca gct gct ggg cca tat	1248
Arg Tyr Arg Leu Thr Lys Ile Ala Val Asp Thr Ala Ala Gly Pro Tyr	
405 410 415	
cag aat cac act gtg gtt ttt ctg gga tca gag aag gga atc atc ttg	1296
Gln Asn His Thr Val Val Phe Leu Gly Ser Glu Lys Gly Ile Ile Leu	
420 425 430	
aag ttt ttg gcc aga ata gga aat agt ggt ttt cta aat gac agc ctt	1344
Lys Phe Leu Ala Arg Ile Gly Asn Ser Gly Phe Leu Asn Asp Ser Leu	
435 440 445	
ttc ctg gag gag atg agt gtt tac aac tct gaa aaa tgc agc tat gat	1392
Phe Leu Glu Glu Met Ser Val Tyr Asn Ser Glu Lys Cys Ser Tyr Asp	
450 455 460	
gga gtc gaa gac aaa agg atc atg ggc atg cag ctg gac aga gca agc	1440
Gly Val Glu Asp Lys Arg Ile Met Gly Met Gln Leu Asp Arg Ala Ser	
465 470 475 480	
agc tct ctg tat gtt gcg ttc tct acc tgt gtg ata aag gtt ccc ctt	1488
Ser Ser Leu Tyr Val Ala Phe Ser Thr Cys Val Ile Lys Val Pro Leu	
485 490 495	
ggc cgg tgt gaa cga cat ggg aag tgt aaa aaa acc tgt att gcc tcc	1536
Gly Arg Cys Glu Arg His Gly Lys Cys Lys Lys Thr Cys Ile Ala Ser	
500 505 510	
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Arg Asp Pro Tyr Cys Gly Trp Ile Lys Glu Gly Gly Ala Cys Ser His	
515 520 525	
tta tca ccc aac agc aga ctg act ttt gag cag gac ata gag cgt ggc	1632
Leu Ser Pro Asn Ser Arg Leu Thr Phe Glu Gln Asp Ile Glu Arg Gly	
530 535 540	
aat aca gat ggt ctg ggg gac tgt cac aat tcc ttt gtg gca ctg aat	1680
Asn Thr Asp Gly Leu Gly Asp Cys His Asn Ser Phe Val Ala Leu Asn	
545 550 555 560	
ggg cat tcc agt tcc ctc ttg ccc agc aca acc aca tca gat tcg acg	1728
Gly His Ser Ser Ser Leu Leu Pro Ser Thr Thr Thr Ser Asp Ser Thr	

565	570	575	
gct caa gag ggg tat gag tct agg gga gga atg ctg gac tgg aag cat			1776
Ala Gln Glu Gly Tyr Glu Ser Arg Gly Gly Met Leu Asp Trp Lys His			
580	585	590	
ctg ctt gac tca cct gac agc aca gac cct ttg ggg gca gtg tct tcc			1824
Leu Leu Asp Ser Pro Asp Ser Thr Asp Pro Leu Gly Ala Val Ser Ser			
595	600	605	
cat aat cac caa gac aag aag gga gtg att cgg gaa agt tac ctc aaa			1872
His Asn His Gln Asp Lys Lys Gly Val Ile Arg Glu Ser Tyr Leu Lys			
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ggc cac gac cag ctc gag			1890
Gly His Asp Gln Leu Glu			
625	630		
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Asn Tyr Thr Lys Gln Tyr Pro Val Phe Val Gly His Lys Pro Gly Arg			
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Asn Thr Thr Gln Arg His Arg Leu Asp Ile Gln Met Ile Met Ile Met			
35	40	45	
Asn Gly Thr Leu Tyr Ile Ala Ala Arg Asp His Ile Tyr Thr Val Asp			
50	55	60	
Ile Asp Thr Ser His Thr Glu Glu Ile Tyr Cys Ser Lys Lys Leu Thr			
65	70	75	80
Trp Lys Ser Arg Gln Ala Asp Val Asp Thr Cys Arg Met Lys Gly Lys			
85	90	95	
His Lys Asp Glu Cys His Asn Phe Ile Lys Val Leu Leu Lys Lys Asn			
100	105	110	
Asp Asp Ala Leu Phe Val Cys Gly Thr Asn Ala Phe Asn Pro Ser Cys			
115	120	125	
Arg Asn Tyr Lys Met Asp Thr Leu Glu Pro Phe Gly Asp Glu Phe Ser			
130	135	140	
Gly Met Ala Arg Cys Pro Tyr Asp Ala Lys His Ala Asn Val Ala Leu			
145	150	155	160
Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr Val Thr Asp Phe Leu Ala			
165	170	175	

Ile	Asp	Ala	Val	Ile	Tyr	Arg	Ser	Leu	Gly	Glu	Ser	Pro	Thr	Leu	Arg	180	185	190
Thr	Val	Lys	His	Asp	Ser	Lys	Trp	Leu	Lys	Glu	Pro	Tyr	Phe	Val	Gln	195	200	205
Ala	Val	Asp	Tyr	Gly	Asp	Tyr	Ile	Tyr	Phe	Phe	Phe	Arg	Glu	Ile	Ala	210	215	220
Val	Glu	Tyr	Asn	Thr	Met	Gly	Lys	Val	Val	Phe	Pro	Arg	Val	Ala	Gln	225	230	235
Val	Cys	Lys	Asn	Asp	Met	Gly	Gly	Ser	Gln	Arg	Val	Leu	Glu	Lys	Gln	245	250	255
Trp	Thr	Ser	Phe	Leu	Lys	Ala	Arg	Leu	Asn	Cys	Ser	Val	Pro	Gly	Asp	260	265	270
Ser	His	Phe	Tyr	Phe	Asn	Ile	Leu	Gln	Ala	Val	Thr	Asp	Val	Ile	Arg	275	280	285
Ile	Asn	Gly	Arg	Asp	Val	Val	Leu	Ala	Thr	Phe	Ser	Thr	Pro	Tyr	Asn	290	295	300
Ser	Ile	Pro	Gly	Ser	Ala	Val	Cys	Ala	Tyr	Asp	Met	Leu	Asp	Ile	Ala	305	310	315
Ser	Val	Phe	Thr	Gly	Arg	Phe	Lys	Glu	Gln	Lys	Ser	Pro	Asp	Ser	Thr	325	330	335
Trp	Thr	Pro	Val	Pro	Asp	Glu	Arg	Val	Pro	Lys	Pro	Arg	Pro	Gly	Cys	340	345	350
Cys	Ala	Gly	Ser	Ser	Ser	Leu	Glu	Arg	Tyr	Ala	Thr	Ser	Asn	Glu	Phe	355	360	365
Pro	Asp	Asp	Thr	Leu	Asn	Phe	Ile	Lys	Thr	His	Pro	Leu	Met	Asp	Glu	370	375	380
Ala	Val	Pro	Ser	Ile	Phe	Asn	Arg	Pro	Trp	Phe	Leu	Arg	Thr	Met	Val	385	390	395
Arg	Tyr	Arg	Leu	Thr	Lys	Ile	Ala	Val	Asp	Thr	Ala	Ala	Gly	Pro	Tyr	405	410	415
Gln	Asn	His	Thr	Val	Val	Phe	Leu	Gly	Ser	Glu	Lys	Gly	Ile	Ile	Leu	420	425	430
Lys	Phe	Leu	Ala	Arg	Ile	Gly	Asn	Ser	Gly	Phe	Leu	Asn	Asp	Ser	Leu	435	440	445
Phe	Leu	Glu	Glu	Met	Ser	Val	Tyr	Asn	Ser	Glu	Lys	Cys	Ser	Tyr	Asp	450	455	460
Gly	Val	Glu	Asp	Lys	Arg	Ile	Met	Gly	Met	Gln	Leu	Asp	Arg	Ala	Ser	465	470	475
																		480

Ser Ser Leu Tyr Val Ala Phe Ser Thr Cys Val Ile Lys Val Pro Leu
 485 490 495
 Gly Arg Cys Glu Arg His Gly Lys Cys Lys Lys Thr Cys Ile Ala Ser
 500 505 510
 Arg Asp Pro Tyr Cys Gly Trp Ile Lys Glu Gly Gly Ala Cys Ser His
 515 520 525
 Leu Ser Pro Asn Ser Arg Leu Thr Phe Glu Gln Asp Ile Glu Arg Gly
 530 535 540
 Asn Thr Asp Gly Leu Gly Asp Cys His Asn Ser Phe Val Ala Leu Asn
 545 550 555 560
 Gly His Ser Ser Ser Leu Leu Pro Ser Thr Thr Thr Ser Asp Ser Thr
 565 570 575
 Ala Gln Glu Gly Tyr Glu Ser Arg Gly Gly Met Leu Asp Trp Lys His
 580 585 590
 Leu Leu Asp Ser Pro Asp Ser Thr Asp Pro Leu Gly Ala Val Ser Ser
 595 600 605
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 atggagaaca acatccagat gatccaggcc gacaccttcc gccacctcca ccacctggag 180
 gtcctgcagt tgggcaggaa ctccatccgg cagattgagg tgggggcctt caacggcctg 240
 gccagcctca acaccctgga gctgttcgac aactggctga cagtcatccc tagcggggcc 300
 tttgaatacc tgtccaagct gcgggagctc tggcttcgca acaaccccat cgaaagcatc 360
 ccctcttacg tcttcaaccg ggtgccctcc ctcatgcgcc tggacttggg ggagctcaag 420
 aagctggagt atatctctga gggagctttt gaggggctgt tcaacctcaa gtatctgaac 480
 ttgggcatgt gcaacattaa agacatgccc aatctcacc cctgggtggg gctggaggag 540
 ctggagatgt cagggaacca ctccctgag atcaggcctg gctccttcca tggcctgagc 600
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 gacgggctgg cttaacttgt ggaactcaac ttggcccaca ataacctctc ttctttgccc 720
 catgacctct ttaccccgct gaggtacctg gtggagttgc atctacacca caacccttgg 780
 aactgtgatt gtgacattct gtggctagcc tgggtggcttc gagagtatat accaccaat 840
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 gtggaccagg cctccttcca gtgctctgcc cccttcatca tggacgcacc tcgagacctc 960
 aacatttctg agggtcggat ggcagaactt aagtgtcgga ctccccctat gtctcctg 1020
 aagtggttgc tgcccaatgg gacagtgcct agccatgcct cccgccacc aaggatctct 1080


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gtcctcaacg acggcacctt gaacttttcc cacgtgctgc tttcagacac cggggtgtac 1140
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acggctgagc ttaacacctc caactacagc ttcttcacca cagtaacagt ggagaccacg 1260
gagatctcgc ctgaggacac aacgcgaaag tacaagcctg ttcctaccac gtccactggg 1320
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<210> 32
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<212> PRT
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<400> 32

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Cys Thr Arg Arg Gly Leu Ser Glu Val Pro Gln Gly Ile Pro Ser Asn
      20             25             30

Thr Arg Tyr Leu Asn Leu Met Glu Asn Asn Ile Gln Met Ile Gln Ala
    35             40             45

Asp Thr Phe Arg His Leu His His Leu Glu Val Leu Gln Leu Gly Arg
    50             55             60

Asn Ser Ile Arg Gln Ile Glu Val Gly Ala Phe Asn Gly Leu Ala Ser
    65             70             75             80

Leu Asn Thr Leu Glu Leu Phe Asp Asn Trp Leu Thr Val Ile Pro Ser
      85             90             95

Gly Ala Phe Glu Tyr Leu Ser Lys Leu Arg Glu Leu Trp Leu Arg Asn
    100             105             110

Asn Pro Ile Glu Ser Ile Pro Ser Tyr Ala Phe Asn Arg Val Pro Ser
    115             120             125

Leu Met Arg Leu Asp Leu Gly Glu Leu Lys Lys Leu Glu Tyr Ile Ser
    130             135             140

Glu Gly Ala Phe Glu Gly Leu Phe Asn Leu Lys Tyr Leu Asn Leu Gly
    145             150             155             160

Met Cys Asn Ile Lys Asp Met Pro Asn Leu Thr Pro Leu Val Gly Leu
      165             170             175

Glu Glu Leu Glu Met Ser Gly Asn His Phe Pro Glu Ile Arg Pro Gly
    180             185             190

Ser Phe His Gly Leu Ser Ser Leu Lys Lys Leu Trp Val Met Asn Ser
    195             200             205

Gln Val Ser Leu Ile Glu Arg Asn Ala Phe Asp Gly Leu Ala Ser Leu
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Val Glu Leu Asn Leu Ala His Asn Asn Leu Ser Ser Leu Pro His Asp
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<220>
<223> Description of Artificial Sequence: Primer

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<220>
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<220>
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<400> 39
ccatattgtg gatggataa 19

<210> 40
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<210> 41
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<220>
<223> Description of Artificial Sequence: Primer

<400> 41
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<210> 42
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<400> 57
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<400> 58
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<210> 60
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<220>
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<400> 60
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<400> 63
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<210> 64
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<400> 64
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<400> 65
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<210> 66
<211> 20
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<400> 66
cctgcgcaaa aagttgtgaa 20

<210> 67
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 <400> 67
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 <400> 69
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 <400> 70
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 <400> 71
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 <210> 72

<211> 18
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<220>
<223> Description of Artificial Sequence: Primer

<400> 72
gctcccgttc cctctcca 18

<210> 73
<211> 31
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 73
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<210> 74
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<212> DNA
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<220>
<221> misc_feature
<222> (1139)..(1172)
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gac aca cct acc atg cgg aca ctc ttc aac ctc ctc tgg ctt gcc ctg 96
Asp Thr Pro Thr Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu
20 25 30

gcc tgc agc cct gtt cac act acc ctg tca aag tca gat gcc aaa aaa 144
Ala Cys Ser Pro Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys
35 40 45

gcc gcc tca aag acg ctg ctg gag aag agt cag ttt tca gat aag ccg 192
Ala Ala Ser Lys Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro
50 55 60

gtg caa gac cgg ggt ttg gtg gtg acg gac ctc aaa gct gag agt gtg 240
Val Gln Asp Arg Gly Leu Val Val Thr Asp Leu Lys Ala Glu Ser Val
65 70 75 80

gtt ctt gag cat cgc agc tac tgc tcg gca aag gcc cgg gac aga cac	288
Val Leu Glu His Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp Arg His	
85 90 95	
ttt gct ggg gat gta ctg ggc tat gtc act cca tgg aac agc cat ggc	336
Phe Ala Gly Asp Val Leu Gly Tyr Val Thr Pro Trp Asn Ser His Gly	
100 105 110	
tac gat gtc acc aag gtc ttt ggg agc aag ttc aca cag atc tca ccc	384
Tyr Asp Val Thr Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro	
115 120 125	
gtc tgg ctg cag ctg aag aga cgt ggc cgt gag atg ttt gag gtc acg	432
Val Trp Leu Gln Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr	
130 135 140	
ggc ctc cac gac gtg gac caa ggg tgg atg cga gct gtc agg aag cat	480
Gly Leu His Asp Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His	
145 150 155 160	
gcc aag ggc ctg cac ata gtg cct cgg ctc ctg ttt gag gac tgg act	528
Ala Lys Gly Leu His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr	
165 170 175	
tac gat gat ttc cgg aac gtc tta gac agt gag gat gag ata gag gag	576
Tyr Asp Asp Phe Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu	
180 185 190	
ctg agc aag acc gtg gtc cag gtg gca aag aac cag cat ttc gat ggc	624
Leu Ser Lys Thr Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly	
195 200 205	
ttc gtg gtg gag gtc tgg aac cag ctg cta agc cag aag cgc gtg ggc	672
Phe Val Val Glu Val Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly	
210 215 220	
ctc atc cac atg ctc acc cac ttg gcc gag gct ctg cac cag gcc cgg	720
Leu Ile His Met Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg	
225 230 235 240	
ctg ctg gcc ctc ctg gtc atc ccg cct gcc atc acc ccc ggg acc gac	768
Leu Leu Ala Leu Leu Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp	
245 250 255	
cag ctg ggc atg ttc acg cac aag gag ttt gag cag ctg gcc ccc gtg	816
Gln Leu Gly Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val	
260 265 270	
ctg gat ggt ttc agc ctc atg acc tac gac tac gca aca ctg tcc tgg	864
Leu Asp Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ala Thr Leu Ser Trp	
275 280 285	
gtt cga gcc tgc gtc cag gtc ctg gat ccc tgg ggc tca act tct atg	912
Val Arg Ala Cys Val Gln Val Leu Asp Pro Trp Gly Ser Thr Ser Met	
290 295 300	

gta tgg act acg cga cct cca agg atg ccc gtg agc ctg ttg tcg ggg 960
 Val Trp Thr Thr Arg Pro Pro Arg Met Pro Val Ser Leu Leu Ser Gly
 305 310 315 320

cca ggt aca tcc aga cac tgaaggacca caggccccgg atggtgtggg 1008
 Pro Gly Thr Ser Arg His
 325

acggccaggc ctcagagcac ttcttcgagt acaagaagag ccgcagtggg aggcacgtcg 1068
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<210> 75
 <211> 326
 <212> PRT
 <213> Homo sapiens

<400> 75

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Asp Thr Pro Thr Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu
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Ala Cys Ser Pro Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys
 35 40 45

Ala Ala Ser Lys Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro
 50 55 60

Val Gln Asp Arg Gly Leu Val Val Thr Asp Leu Lys Ala Glu Ser Val
 65 70 75 80

Val Leu Glu His Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp Arg His
 85 90 95

Phe Ala Gly Asp Val Leu Gly Tyr Val Thr Pro Trp Asn Ser His Gly
 100 105 110

Tyr Asp Val Thr Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro
 115 120 125

Val Trp Leu Gln Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr
 130 135 140

Gly Leu His Asp Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His
 145 150 155 160

Ala Lys Gly Leu His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr
 165 170 175

Tyr Asp Asp Phe Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu
 180 185 190
 Leu Ser Lys Thr Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly
 195 200 205
 Phe Val Val Glu Val Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly
 210 215 220
 Leu Ile His Met Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg
 225 230 235 240
 Leu Leu Ala Leu Leu Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp
 245 250 255
 Gln Leu Gly Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val
 260 265 270
 Leu Asp Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ala Thr Leu Ser Trp
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 Val Arg Ala Cys Val Gln Val Leu Asp Pro Trp Gly Ser Thr Ser Met
 290 295 300
 Val Trp Thr Thr Arg Pro Pro Arg Met Pro Val Ser Leu Leu Ser Gly
 305 310 315 320
 Pro Gly Thr Ser Arg His
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 ctgtcaaagt cagatgccaa aaaagccgcc tcaaagacgc tgctggagaa gagtcagttt 180
 tcagataagc cgggtgaaga ccgggggtttg gtggtgacgg acctcaaagc tgagagtgtg 240
 gttcttgagc atgcagcta ctgctcggca aaggcccggg acagacactt tgctgggg 298

atg tac tgg gct atg tca ctc cac cag tgg aac agc cat ggc tac gat	346
Met Tyr Trp Ala Met Ser Leu His Gln Trp Asn Ser His Gly Tyr Asp	
1 5 10 15	
gtc acc aag gtc ttt ggg agc aag ttc aca cag atc tca ccc gtc tgg	394
Val Thr Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val Trp	
20 25 30	
ctg cag ctg aag aga cgt ggc cgt gag atg ttt gag gtc acg ggc ctc	442
Leu Gln Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr Gly Leu	
35 40 45	
cac gac gtg gac caa ggg tgg atg cga gct gtc agg aag cat gcc aag	490
His Asp Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys	
50 55 60	
ggc ctg cac ata gtg cct cgg ctc ctg ttt gag gac tgg act tac gat	538
Gly Leu His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr Asp	
65 70 75 80	
gat ttc cgg aac gtc tta gac agt gag gat gag ata gag gag ctg agc	586
Asp Phe Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu Ser	
85 90 95	
aag acc gtg gtc cag gtg gca aag aac cag cat ttc gat ggc ttc gtg	634
Lys Thr Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe Val	
100 105 110	
gtg gag gtc tgg aac cag ctg cta agc cag aag cgc gtg ggc ctc atc	682
Val Glu Val Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly Leu Ile	
115 120 125	
cac atg ctc acc cac ttg gcc gag gct ctg cac cag gcc cgg ctg ctg	730
His Met Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg Leu Leu	
130 135 140	
gcc ctc ctg gtc atc ccg cct gcc atc acc ccc ggg acc gac cag ctg	778
Ala Leu Leu Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp Gln Leu	
145 150 155 160	
ggc atg ttc acg cac aag gag ttt gag cag ctg gcc ccc gtg ctg gat	826
Gly Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val Leu Asp	
165 170 175	
ggt ttc agc ctc atg acc tac gac tac gca aca ctg tcc tgg gtt cga	874
Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ala Thr Leu Ser Trp Val Arg	
180 185 190	
gcc tgc gtc cag gtc ctg gat ccc tgg ggc tca act tct atg gta tgg	922
Ala Cys Val Gln Val Leu Asp Pro Trp Gly Ser Thr Ser Met Val Trp	
195 200 205	
act acg cga cct cca agg atg ccc gtg agc ctg ttg tcg ggg cca ggt	970
Thr Thr Arg Pro Pro Arg Met Pro Val Ser Leu Leu Ser Gly Pro Gly	
210 215 220	

aca tcc aga cac tgaaggacca caggccccgg atggtgtggg acggccaggc 1022
 Thr Ser Arg His
 225

ctcagagcac ttcttcgagt acaagaagag ccgcagtggg aggcacgtcg tcttctaccc 1082
 aaccctgaag tccctgcagg tgcggctgga gctggcccgg gagctgggcg ttgggggtctc 1142
 natntgggag ctgggccagg gcctggacta cttntacgac ctgctctagg tgggcattgc 1202
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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 His Asp Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys
 50 55 60
 Gly Leu His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr Asp
 65 70 75 80
 Asp Phe Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu Ser
 85 90 95
 Lys Thr Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe Val
 100 105 110
 Val Glu Val Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly Leu Ile
 115 120 125
 His Met Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg Leu Leu
 130 135 140
 Ala Leu Leu Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp Gln Leu
 145 150 155 160
 Gly Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val Leu Asp
 165 170 175
 Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ala Thr Leu Ser Trp Val Arg
 180 185 190

Ala Cys Val Gln Val Leu Asp Pro Trp Gly Ser Thr Ser Met Val Trp
195 200 205

Thr Thr Arg Pro Pro Arg Met Pro Val Ser Leu Leu Ser Gly Pro Gly
210 215 220

Thr Ser Arg His
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<210> 78
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<212> DNA
<213> Homo sapiens

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ccg gcc gcg tgg ggg cgc gcc agg gag aat atc tgc ttg ctc aac ttt 97
Pro Ala Ala Trp Gly Arg Ala Arg Glu Asn Ile Cys Leu Leu Asn Phe
20 25 30

ttc tgt ggc acc atc gtg ctc atc ttc ttc ctg gag ctg gct gtg gcc 145
Phe Cys Gly Thr Ile Val Leu Ile Phe Phe Leu Glu Leu Ala Val Ala
35 40 45

gtg ctg gcc ttc ctg ttc cag gac tgg gtg agg gac cgg ttc cgg gag 193
Val Leu Ala Phe Leu Phe Gln Asp Trp Val Arg Asp Arg Phe Arg Glu
50 55 60

ttc ttc gag agc aac atc aag tcc tac cgg gac gat atc gat ctg caa 241
Phe Phe Glu Ser Asn Ile Lys Ser Tyr Arg Asp Asp Ile Asp Leu Gln
65 70 75 80

aac ctc atc gac tcc ctt cag aaa gct aac cag tgc tgt ggc gca tat 289
Asn Leu Ile Asp Ser Leu Gln Lys Ala Asn Gln Cys Cys Gly Ala Tyr
85 90 95

ggc cct gaa gac tgg gac ctc aac gtc tac ttc aat tgc agc ggt gcc 337
Gly Pro Glu Asp Trp Asp Leu Asn Val Tyr Phe Asn Cys Ser Gly Ala
100 105 110

agc tac agc cga gag aag tgc ggg gtc ccc ttc tcc tgc tgc gtg cca 385
Ser Tyr Ser Arg Glu Lys Cys Gly Val Pro Phe Ser Cys Cys Val Pro
115 120 125

gat cct gcg caa aaa gtt gtg aac aca cag tgt gga tat gat gtc agg 433
Asp Pro Ala Gln Lys Val Val Asn Thr Gln Cys Gly Tyr Asp Val Arg
130 135 140

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att cag ctg aag agc aag tgg gat gag tcc atc ttc acg aaa ggc tgc 481
Ile Gln Leu Lys Ser Lys Trp Asp Glu Ser Ile Phe Thr Lys Gly Cys
145 150 155 160

atc cag gcg ctg gaa agc tgg ctc ccg cgg aac att tac att gtg gct 529
Ile Gln Ala Leu Glu Ser Trp Leu Pro Arg Asn Ile Tyr Ile Val Ala
165 170 175

ggc gtc ttc atc gcc atc tcg ctg ttg cag ata ttt ggc atc ttc ctg 577
Gly Val Phe Ile Ala Ile Ser Leu Leu Gln Ile Phe Gly Ile Phe Leu
180 185 190

gca agg acg ctg atc tca gac atc gag gca gtg aag gcc ggc cat cac 625
Ala Arg Thr Leu Ile Ser Asp Ile Glu Ala Val Lys Ala Gly His His
195 200 205

ttc tgaggagcag agttgaggga gccgagctga gccacgctgg gaggccagag 678
Phe

cctttctctg ccatcagccc tacgtccaga gggagaggag ccgacacccc cagagccagt 738

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ccaagggtcc cccttggt 816

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<210> 79
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<212> PRT
<213> Homo sapiens

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20 25 30

Phe Cys Gly Thr Ile Val Leu Ile Phe Phe Leu Glu Leu Ala Val Ala
35 40 45

Val Leu Ala Phe Leu Phe Gln Asp Trp Val Arg Asp Arg Phe Arg Glu
50 55 60

Phe Phe Glu Ser Asn Ile Lys Ser Tyr Arg Asp Asp Ile Asp Leu Gln
65 70 75 80

Asn Leu Ile Asp Ser Leu Gln Lys Ala Asn Gln Cys Cys Gly Ala Tyr
85 90 95

Gly Pro Glu Asp Trp Asp Leu Asn Val Tyr Phe Asn Cys Ser Gly Ala
100 105 110

Ser Tyr Ser Arg Glu Lys Cys Gly Val Pro Phe Ser Cys Cys Val Pro
115 120 125

Asp Pro Ala Gln Lys Val Val Asn Thr Gln Cys Gly Tyr Asp Val Arg

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130	135	140
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145 . 150 155 160		
Ile Gln Ala Leu Glu Ser Trp Leu Pro Arg Asn Ile Tyr Ile Val Ala		
165 170 175		
Gly Val Phe Ile Ala Ile Ser Leu Leu Gln Ile Phe Gly Ile Phe Leu		
180 185 190		
Ala Arg Thr Leu Ile Ser Asp Ile Glu Ala Val Lys Ala Gly His His		
195 200 205		

Phe

<210> 80
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 <213> Homo sapiens

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Met Ser Asn Pro Ser Ala Pro Pro Pro Tyr Glu Asp Arg Asn Pro	
1 5 10 15	

ctg tac cca ggc cct ctg ccc cct ggg ggc tat ggg cag cca tct gtc	155
Leu Tyr Pro Gly Pro Leu Pro Pro Gly Gly Tyr Gly Gln Pro Ser Val	
20 25 30	

ctg cca gga ggg tat cct gcc tac cct ggc tac ccg cag cct ggc tac	203
Leu Pro Gly Gly Tyr Pro Ala Tyr Pro Gly Tyr Pro Gln Pro Gly Tyr	
35 40 45	

ggt cac cct gct ggc tac cca cag ccc atg ccc ccc acc cac ccg atg	251
Gly His Pro Ala Gly Tyr Pro Gln Pro Met Pro Pro Thr His Pro Met	
50 55 60	

ccc atg aac tac ggc cca ggc cat ggc tat gat ggg gag gag aga gcg	299
Pro Met Asn Tyr Gly Pro Gly His Gly Tyr Asp Gly Glu Glu Arg Ala	
65 70 75	

gtg agt gat agc ttc ggg cct gga gag tgg gat gac cgg aaa gtg cga	347
Val Ser Asp Ser Phe Gly Pro Gly Glu Trp Asp Asp Arg Lys Val Arg	
80 85 90 95	

cac act ttt atc cga aag gtt tac tcc atc atc tcc gtg cag ctg ctc	395
His Thr Phe Ile Arg Lys Val Tyr Ser Ile Ile Ser Val Gln Leu Leu	

100										105										110										
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Ile	Thr	Val	Ala	Ile	Ile	Ala	Ile	Phe	Thr	Phe	Val	Glu	Pro	Val	Ser															
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Ala	Phe	Val	Arg	Arg	Asn	Val	Ala	Val	Tyr	Tyr	Val	Ser	Tyr	Ala	Val															
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Phe	Val	Val	Thr	Tyr	Leu	Ile	Leu	Ala	Cys	Cys	Gln	Gly	Pro	Arg	Arg															
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210					215					220																				
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225					230					235																				
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Phe	Pro	Arg	Asp	Leu	Ile	Pro	Phe	Ser	Ser	Ser	Ala	Pro	Thr	Lys	Leu															
240	245					250					255																			
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Cys	Pro	Val	Ser	Val	Leu	Arg	Met	Leu	Trp	Thr	Phe	Pro	Tyr	Pro	Leu															
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275					280					285																				
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Cys	His	Ser	His	Leu	Thr	Gly	Ala	Ser	Phe	Leu	Leu	Pro	Gly	Arg	Trp															
290					295					300																				
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305					310					315																				
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Trp																														
320																														

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2574

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 <211> 320
 <212> PRT

<213> Homo sapiens

<400> 81

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Pro	Gly	Gly	Tyr	Pro	Ala	Tyr	Pro	Gly	Tyr	Pro	Gln	Pro	Gly	Tyr	Gly	
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His	Pro	Ala	Gly	Tyr	Pro	Gln	Pro	Met	Pro	Pro	Thr	His	Pro	Met	Pro	
	50					55					60					
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Ser	Asp	Ser	Phe	Gly	Pro	Gly	Glu	Trp	Asp	Asp	Arg	Lys	Val	Arg	His	
				85					90					95		
Thr	Phe	Ile	Arg	Lys	Val	Tyr	Ser	Ile	Ile	Ser	Val	Gln	Leu	Leu	Ile	
			100					105					110			
Thr	Val	Ala	Ile	Ile	Ala	Ile	Phe	Thr	Phe	Val	Glu	Pro	Val	Ser	Ala	
		115					120					125				
Phe	Val	Arg	Arg	Asn	Val	Ala	Val	Tyr	Tyr	Val	Ser	Tyr	Ala	Val	Phe	
	130					135					140					
Val	Val	Thr	Tyr	Leu	Ile	Leu	Ala	Cys	Cys	Gln	Gly	Pro	Arg	Arg	Arg	
145					150					155					160	
Phe	Pro	Trp	Asn	Ile	Ile	Leu	Leu	Thr	Leu	Phe	Thr	Phe	Ala	Met	Gly	
				165					170					175		
Phe	Met	Thr	Gly	Thr	Ile	Ser	Ser	Met	Tyr	Gln	Thr	Lys	Ala	Val	Ile	
			180					185					190			
Ile	Ala	Met	Ile	Ile	Thr	Ala	Val	Val	Ser	Ile	Ser	Val	Thr	Ile	Phe	
		195					200					205				
Cys	Phe	Gln	Thr	Lys	Val	Arg	Ala	Trp	Arg	Ala	Leu	Pro	Trp	Pro	Pro	
	210					215					220					
Asp	Ser	Pro	Phe	Leu	Ser	Gly	Pro	Asp	Pro	Gly	Thr	Leu	Gly	Met	Phe	
225					230					235					240	
Pro	Arg	Asp	Leu	Ile	Pro	Phe	Ser	Ser	Ser	Ala	Pro	Thr	Lys	Leu	Cys	
			245						250					255		
Pro	Val	Ser	Val	Leu	Arg	Met	Leu	Trp	Thr	Phe	Pro	Tyr	Pro	Leu	Gly	
			260					265					270			
Gly	Ser	Thr	Gly	Thr	Pro	Trp	Gln	Gly	Gln	Ser	Asp	Trp	Ala	Gly	Cys	
		275					280					285				

His Ser His Leu Thr Gly Ala Ser Phe Leu Leu Pro Gly Arg Trp Thr
290 295 300

Ser Pro Arg Ala Gln Ala Ser Ser Val Ser Trp Glu Leu Cys Ser Trp
305 310 315 320